

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.  
 \*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.  
 Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or  
 utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if  
 known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\*: Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the  
 appropriate serial number.

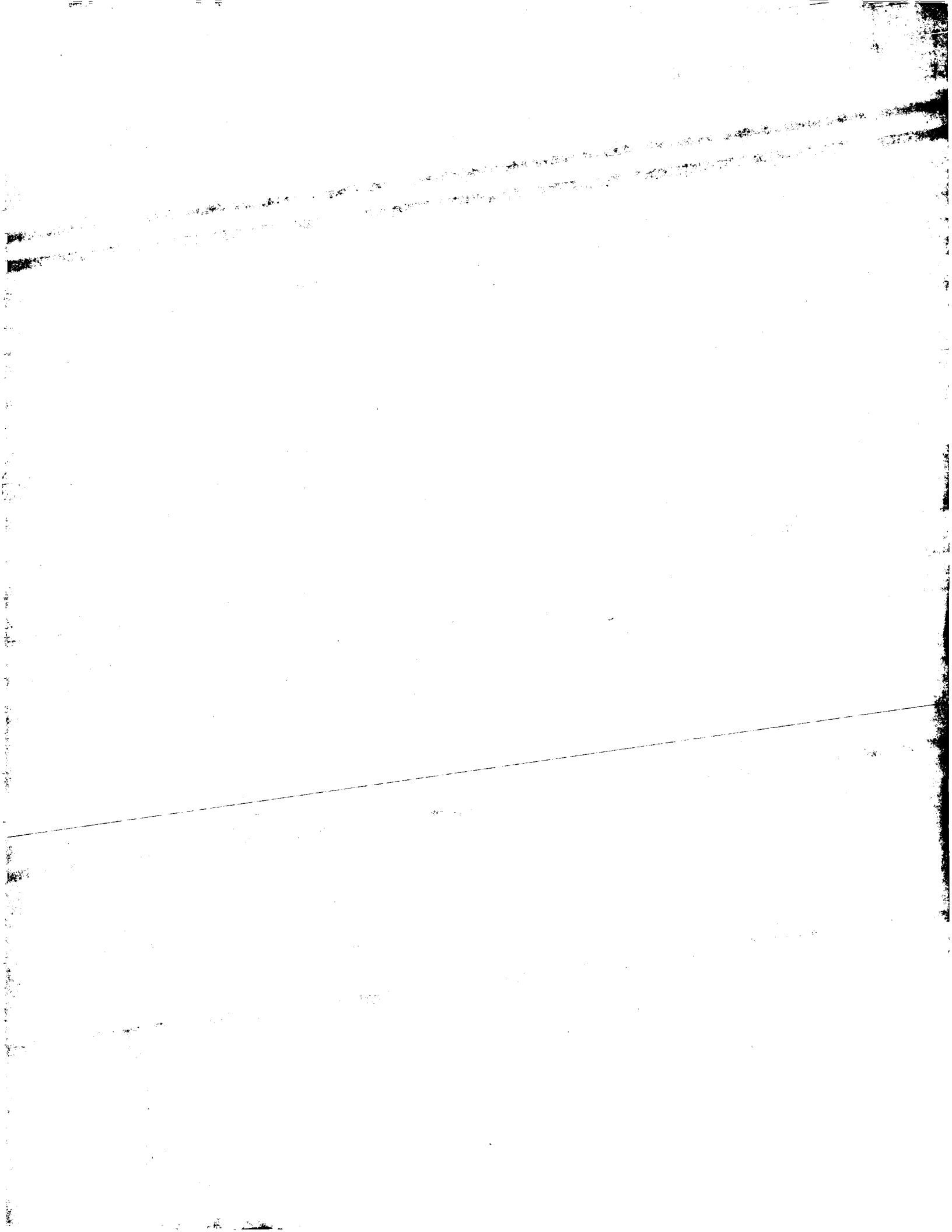
Jan Delaval  
 Reference Librarian  
 Biotechnology & Chemical Library  
 CM1 1E07 - 703-308-4498  
 jan.delaval@uspto.gov

## STAFF USE ONLY

## Type of Search

## Vendors and cost where applicable

Searcher: Jan NA Sequence (#) ✓ STN \_\_\_\_\_  
 Searcher Phone #: 444 AA Sequence (#) ✓ Dialog \_\_\_\_\_  
 Searcher Location: \_\_\_\_\_ Structure (#) \_\_\_\_\_ Questel/Orbit \_\_\_\_\_  
 Date Searcher Picked Up: 5/26/02 Bibliographic \_\_\_\_\_ Dr. Link \_\_\_\_\_  
 Date Completed: 5/26/02 Litigation \_\_\_\_\_ Lexis/Nexis \_\_\_\_\_  
 Searcher Prep & Review Time: \_\_\_\_\_ Fulltext \_\_\_\_\_ Sequence Systems ✓  
 Clerical Prep Time: 15 Patent Family \_\_\_\_\_ WWW/Internet \_\_\_\_\_  
 Online Time: 15 Other \_\_\_\_\_ Other (specify) \_\_\_\_\_



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:00:21 ; Search time 1863.47 Seconds  
(without alignments)  
4548.100 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 1 atgggttggaactgtatcat.....cccttgcaccgtctctca 405

Sequence: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues 3595312

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
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10: gb\_ro:\*  
11: gb\_sts:\*  
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31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query #  
No. Score Match Length DB ID Description

## SUMMARIES

1	289.6	71.5	805	12	AF239196	AF239196 Synthetic
2	272.2	67.2	446	6	I08288	I08288 Sequence 4
3	272.2	67.2	462	10	S78361	S78361 AHT107 VH r
4	265.8	65.6	1767	6	E40699	E40699 Antihuman F
5	265.8	65.6	1768	6	E40700	E40700 Antihuman F
6	254.4	62.8	424	6	AR174947	AR174947 Sequence
7	253.6	62.6	451	6	AR144016	AR144016 Sequence
8	253.6	62.6	2071	6	E40080	E40080 Drug contai
9	253.6	62.6	2071	6	E40888	E40888 Humanized a
10	253.6	62.6	2071	6	E43434	E43434 Humanized a
11	252	62.2	2073	6	E40910	E40910 Humanized a
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14	250.4	61.8	2073	6	E40912	E40912 Humanized a
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16	248.8	61.4	457	6	E40850	E40850 Humanized a
17	248.8	61.4	457	6	E43396	E43396 Humanized a
18	248.8	61.4	2077	6	E40055	E40055 Drug contai
19	248.8	61.4	2077	6	E40863	E40863 Humanized a
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21	248.2	61.3	433	6	AR024343	AR024343 Sequence
22	248.2	61.3	433	6	AR045196	AR045196 Sequence
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24	248.2	61.3	433	6	E43890	E43890 Chimeric an
25	245.6	60.6	2077	6	E43441	E43441 Humanized a
26	245	60.5	405	6	AR126855	AR126855 Sequence
27	245	60.5	405	6	I31950	I31950 Sequence 68
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29	245	60.5	405	6	I78617	I78617 Sequence 68
30	245	60.5	405	9	HSBUD114H	Z46348 Homo sapien
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32	243.4	60.1	405	6	E16346	E16346 DNA encodin
33	243.4	60.1	1773	6	E14571	E14571 Mouse mRNA
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35	241.8	59.7	414	9	AF062257	AF062257 Homo sapi
36	241.8	59.7	451	10	MUSANTYDJ	M37621 Mouse anti-
37	241.8	59.7	471	10	MUSIGHPG	M27788 Mouse Ig ac
38	241.2	59.6	700	10	MUSIGHAQ	M00494 Mouse Ig ac
39	241.2	59.6	700	10	MUSIGHAM	M25465 Mouse Ig re
40	240.2	59.3	402	9	HSVH1B6	Z47222 H. sapiens m
41	240.2	59.3	406	10	MUSIGHMX	M28251 Mouse Ig re
42	240.2	59.3	443	6	I09505	I09505 Sequence 3
43	239.2	59.1	466	10	MMIGRF24	X14623 Murine MRL-
44	239	59.0	418	6	E16328	E16328 DNA coding
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## ALIGNMENTS

RESULT 1  
AF239196 LOCUS 805 bp. mRNA linear SYN 03-JUL-2000  
DEFINITION Synthetic construct BCL1 lymphoma-derived single chain idliotype  
ACCESSION AF239196  
VERSION AF239196.1 GI:8925314  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM artificial sequence.  
REFERENCE 1 (bases 1 to 805)  
AUTHORS Schreurs,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and Kersten,M.J.  
TITLE Murine BCL1 lymphoma-derived single chain antibody (scFv) sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 805)  
AUTHORS Schreurs,M.W.J., van den Berk,P.C.M., van Oers,M.H.J. and Kersten,M.J.  
TITLE Direct Submission  
JOURNAL Submitted (24-FEB-2000) Immunology, The Netherlands Cancer  
Institute, Plemanlaan 121, Amsterdam 1066 CX, The Netherlands  
FEATURES Location/Qualifiers

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/tissue\_type="Bcl1 lymphoma"  
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67. .417  
/note="Region: heavy chain variable region"  
misc\_feature  
418. .462  
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463. .792  
/note="Region: lambda light chain V region"  
BASE COUNT 206 a 191 c 206 g 202 t  
ORIGIN

Query Match 71.5%; Score 289.6; DB 12; Length 805;  
Best Local Similarity 83.6%; Pred. No. 1.6e-81;  
Matches 341; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 atgggttggaactgatacatctctctctgtgtacccaagctaaagctgagcctccag 60  
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DB 10 ATGGGTGGAGCTGTATCATCTTCTTCTGTAGTACCAAGCTACAGGTGTGCATCCAC 69  
QY 61 gtccagctgtgagctgagctgagctgagctgagctgagctgagctgagctgagctg 120  
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DB 70 GTCCAGCTGCAGCAGTGTGGGCTGTAGGCTGTAGGCTGTAGGCTGTAGGCTGTAG 129  
QY 121 tgcgaagcttcgcgctacacattcattgatactatacagctgagctgagctgagct 180  
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DB 130 TGCAGAGGCTTCGGCTACATTCATGATTCATGATTCATGATTCATGATTCATG 189  
QY 181 ggcagagcctcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240  
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DB 190 GCAAGAGTGTAGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 249  
QY 241 cagaagcttaagggcagaagccacatgactgtagacaagctgagctgagctgagctgagct 300  
|||||  
DB 250 CAGAAGTGTAAAGGCAAGGCCACATGCTGTAGCAAAATCTCTCACACAGCTTATATG 309  
QY 301 gaacttaagcttcctgagctgagctgagctgagctgagctgagctgagctgagctg 357  
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DB 310 GAACCTGCCAGATTGACATCTGAGAGATTCTGCATCTATTACTGTGCAAGTACTATG 369  
QY 358 tggatatagtactgagctgagctgagctgagctgagctgagctgagctgagctgagct 405  
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DB 370 AACTACTTTGACTACTGTGGGCAAGGCCACCACTCTCTACAGTCTCTCTCA 417

RESULT 2  
LOCUS 108288 446 bp linear PAT 02-DEC-1994  
DEFINITION Sequence 4 from Patent EP 0380068.  
ACCESSION 108288  
VERSION 108288.1 GI:589000  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 446)  
AUTHORS Zerler,B.D.  
TITLE An expression system for production of chimeric monoclonal  
antibodies  
JOURNAL Patent: EP 0380068-A1 4 01-AUG-1990;  
FEATURES  
source location/Qualifiers  
1. .446  
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BASE COUNT 117 a 110 c 113 g 106 t  
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Matches 322; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

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QY 61 gtccagctgtgagctgagctgagctgagctgagctgagctgagctgagctgagctg 120  
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QY 121 tgcgaagcttcgcgctacacattcattgatactatacagctgagctgagctgagct 180  
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QY 181 ggcagagcctcgagctgagctgagctgagctgagctgagctgagctgagctgagct 240  
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DB 285 CCGAGGTTTAAAGGCCAAGGCCACATGACTGTACAAATCTCTCACACAGCTTATATG 344  
QY 301 gaacttaagcttcctgagctgagctgagctgagctgagctgagctgagctgagctg 360  
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DB 345 GAACCTGCCAGATTGACATCTGAGAGATTCTGCATCTATTACTGTGCAAGA---GGAAGC 401  
QY 361 tatatgactgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 405  
|||||  
DB 402 AACCTTGACTACTGTGGGCAAGGCCACCACTCTCTACAGTCTCTCTCA 446

RESULT 3  
LOCUS 578361 462 bp mRNA linear ROD 07-MAY-1993  
DEFINITION AHT107 VH region-chimeric mouse/human MAb against the human p55  
IL-2R heavy chain variable region [mice, mRNA Recombinant Partial,  
462 nt].  
ACCESSION 578361  
VERSION 578361.1 GI:243052  
KEYWORDS  
SOURCE  
ORGANISM Mus sp.  
MUS SP.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 462)  
REFERENCE Rose,B., Gillespie,A., Wunderlich,D., Barbosa,J.A., Cahill,K.,  
Dzubia,D., Shedd,D. and Zerler,B.  
TITLE A chimeric mouse/human anti-IL-2 receptor antibody with enhanced  
biological activities  
JOURNAL Mol. Immunol. 29 (1), 131-144 (1992)  
MEDLINE 92114885  
REMARK Genbank staff at the National Library of Medicine created this  
entry [NCBI g1bbsq 78361] from the original journal article.  
This sequence comes from Fig1B.  
location/Qualifiers  
1. .462  
/organism="Mus sp."





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Matches 318;	Conservative	0;	Mismatches 87;	Indels 0; Gaps 0;			
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PC	A61K39/395.A61P29/00.C12N15/09//C07K16/28.C12P21/02.C12N15/00						
CC	Key						
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QY	361	ta---tatggacttactgggtgcaaggtcaacccctgtcacccgtctctca	405
Db	371	tatattatggactattgggtgcaaggtcaacccctgtcacccgtctctctca	418
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DEFINITION	Sequence	11	from patent US 6210671.
ACCESSION	ARI44016		
VERSION	ARI44016.1		GI:15105883
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 451)		
AUTHORS	Co,M,Sung,I		
TITLE	Humanized antibodies reactive with L-selectin		
JOURNAL	Patent: US 6210671-A 11 03-APR-2001;		
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QY	61	gtcccaagctggtgcaactctggggctgaagtgaaagacccctggagagctcaagtgaagtgctcc	120
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QY	181	ggacagggcccttgagttgattggagtttaataattactatgataataatacaatacaaac	240
Db	192	ggacagggcccttgagttgattggagtttaataattactatgataataatacaatacaaac	251
QY	241	cagaagctttaaagggaagccacaatgactgactgagaacaagctgcagacagacagctata	300

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
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81	GTCCAACTGTGTGATCTGTGGGCTCAGGTGCAAGAACGCTGGGGCTTTCAGTGAAGTGTCC	140								
121	tgcaagctctgcgtctaacacaltcactgaltatgctatacagctgtggtgagacagctctc	180								
141	TGCAAGGCTTCTGGCTACACCTTACACGAGCTACTGATGACGTGGTAAACAGGCCCT	200								
181	ggacagggcgctcagtgatgttgatgtatcttaattctacttaataatacaaacacacac	240								
201	GGACAGGGCGCTTGAGTGGATGGAGAGATGATGATCTTGTATGAGCTATACACTACAT	260								
241	cagaagcttaagggagaaagccacaatgactgtgagacaaatcgacagcacagccatactg	300								
261	CAAAAGTTCAAGGCAAGGCCACATTGACTGTAGACACATCATCAGCAAGCAGCCACTAG	320								
301	gaactagttctttagatctgtgagatacagcgcgttatactgtgcaaga-----	351								
321	GAGCTCAGAGCGCTGAGATCTGAGACACAGCGGGCTCTATTACTGTGCAAGAAATAGGAC	380								
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381	TATAGTACACACTGTGACTGTGATGTCTGTGGGCGAAGGAGCCTGTGTCACGCTCTCPCA	440								
RESUT	6									
E40888	E40888	2071 bp	DNA	linear	PAT 31-JAN-2002					
DEFINITION	Humanized anti-Fas antibody.									
ACCESSION	E40888									
VERSION	E40888.1 GI:18627465									
KEYWORDS	JP 2000166574-A/77.									
SOURCE	synthetic construct.									
ORGANISM	synthetic construct									
REFERENCE	artificial sequence.									
AUTHORS	1 (bases 1 to 2071)									
TITLE	Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I.									
JOURNAL	Humanized anti-Fas antibody									
COMMENT	Patent: JP 2000166574-A 77 20-JUN-2000;									
	SANKYO CO LTD									
	OS Artificial Sequence									
	PN JP 2000166574-A/77									
	PD 20-JUN-2000									
	PF 29-SEP-1999 JP 1999275441									
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	PI NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKURO TAMAKI									
	PC C12N15/09, A61K39/00, A61K39/395, A61K39/395, A61P37/02, A61P43/00,									
	PC C02K16/18,									
	PC C12N1/21, C12N5/10, C12P21/08, (C12N1/21, C12R1:19), C12N15/00, PC									
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CC										
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BASE COUNT      460 a      685 c      561 g      365 t
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 Db 21 atggatgtgagctgattatcatctcttcttcttgtagcacacgctacaggttccacttccag 80  
 Oy 61 gtccagcttggtgcagtlctltgaggcttgagtgaaagccctgggagctcagtgaaagtgltcc 120  
 Db 81 gtccaaactggtgcactctgtgggcttagaggtcagaagaacctgggggcttcactgaaggtgcc 140  
 Oy 121 tgcgaagcttcgggtacacalcacatcgtatatlgtcctatacagltgggtgagacaggtcct 180  
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 Oy 161 ggaacgggctcctgagtgagtttgagttatataattactatagatatatacaactcaac 240  
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LOCUS	E43434	2071 bp	DNA	linear	PAT 31-JAN-2007	
DEFINITION	Humanized anti-Fas antibody.					
ACCESSION	E43434					
VERSION	E43434.1	GI:18627700				
KEYWORDS	JP 2000166573-A/77.					
SOURCE	synthetic construct.					
ORGANISM	artificial sequence.					
	1 (bases 1 to 2071)					
	Takahashi, W., Haruyama, H. and Serizawa, N.					
REFERENCE	Humanized anti-Fas antibody					
AUTHORS	Patent: JP 2000166573-A 77 20-JUN-2000;					
TITLE	SANKYO CO LTD					
JOURNAL	OS Artificial Sequence					
COMMENT	PN	JP 2000166573-A/77				
	PD	20-JUN-2000				
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	PR					
	PI	WATANABE TAKAHASHI, HIDEYUKI HARUYAMA, NOBUKI SERIZAWA PC				
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	A61P43/00,					
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FT exon	(1716) . (2036)
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FT mat peptide	(1126) . (1170)
FT mat peptide	(1289) . (1618)
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QY 61 gtccagctgtgtcaagtlcttggggcttgaggtgaagaagccttggagctcagtgaaagtytcc 120  
DB 81 gtccaaactggtcacgctctggggcttgaggccaagaagccctggggctttcaatgaaagggtccc 140  
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FT intron (173) . (1127)
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Best Local Similarity 77.4%; Pred. No. 2.1e-69;
Matches 325; Conservative 0; Mismatches 80; Indels 15; Gaps 1;
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Db 23 ATGGGATGGAGCTGTATCATCTCTTCTGTGTACACACAGCTACAGGTGTCATTCTCAG 82
QY 61 gtccagctgtgtgcaagctgtgaggtgaggaagcctgtggaagctgaaggtgtcc 120
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QY 301 gaacttagtcttcttgagatctgagatagacgagcgtttattactgtgcaaga----- 351
Db 323 GAGCTCAGCAGCTGAGATCTGAGGACACGGCGGTATTACTGTGCAAGAAATAGGGAC 382
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DEFINITION Humanized anti-Fas antibody.
ACCESSION E40911
VERSION E40911.1 GI:18627488
KEYWORDS JP 2000166574-A/100.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 2073).
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
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TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166574-A 100 20-JUN-2000;
COMMENT SANKYO CO LTD
OS Artificial Sequence
PN JP 2000166574-A/100
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275441
PR NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKURO TAMAKI
PI C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
PC C07K16/18
PC C12N1/21,C12N5/10,C12P21/08/(C12N1/21,C12R1:19),C12N15/00, PC
C12N5/00
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FT exon (1128) . (1172)
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FT exon (1718) . (2038)
FT mat_peptide (80) . (736)
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FT mat_peptide (1291) . (1620)
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 ACCESSION X65893 S59756  
 VERSION X65893.1 GI:395090  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 405)  
 AUTHORS Schiff, C.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedex 9, FRANCE  
 REFERENCE 2 (bases 1 to 405)  
 AUTHORS Millil, M., Le Deist, F., de Saint-Basile, G., Fischer, A., Fougerneau, M. and Schiff, C.  
 TITLE Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like repertoire  
 JOURNAL J Clin. Invest. 91 (4), 1616-1629 (1993)  
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 DEFINITION Humanized anti-Fas antibody.  
 ACCESSION E40912  
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 KEYWORDS JP 2000166574-A/101.  
 SOURCE synthetic construct.  
 ORGANISM artificial sequence.  
 REFERENCE 1 (bases 1 to 2073)  
 AUTHORS Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I.  
 TITLE Humanized anti-Fas antibody  
 JOURNAL Patent: JP 2000166574-A/101 20-JUN-2000;  
 SANKYO CO LTD  
 COMMENT OS Artificial Sequence  
 PN JP 2000166574-A/101  
 PD 20-JUN-2000  
 PF 29-SEP-1999 JP 1999275441  
 PR NOBUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI  
 PI C12N15/09, A61K39/00, A61K39/395, A61P37/02, A61P43/00,  
 PC C07K16/18,  
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 Best local Similarity 77.1%; Pred. No. 6.7e-69;  
 Matches 324; Conservative 0; Mismatches 81; Indels 15; Gaps 1;







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:01:26 ; Search time 2170.14 Seconds

(without alignments)  
2518.854 Million cell updates/sec

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Gap 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em\_estba:\*  
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4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc1:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pin:\*  
16: em\_gss\_vtl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	233.8	57.7	771	10	B140551
7	232	57.3	723	10	BG969577
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26	221.4	54.7	764	10	BG745457	BG745457	602724025
27	221.2	54.6	1576	11	AK007918	AK007918	Mus muscu
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DEFINITION 602829160F1 NCL\_CGAP-Co24 Mus musculus cDNA clone IMAGE:4963974 5',  
mRNA sequence.  
ACCESSION BG965088.1 GI:14352725  
VERSION BG965088  
KEYWORDS house mouse.  
SOURCE Mus musculus.  
ORGANISM Mus musculus.  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE 1 (bases 1 to 738)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LHAM10989 row: g column: 15  
High quality sequence stop: 716.  
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Average insert size 1.6 kb. Constructed by Life  
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BASE COUNT

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Matches 313; Conservative 0; Mismatches 92; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtaccacagctacagtggtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 34 ATGGATGGAGCTGTATCATCTCTCTGTGTACCAACAGCTACAGGTCCACTCCAG 93  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 61 gtccagctggtcagctggtggtggtgaagaagctgtgagctcagtgaaagtgtcc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 94 GTCCAACTGCAGCAGCTGGGGCTGACCTGGTGAACCTGGGGCTTCACTGAAGTTGTCC 153  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 121 tgcnaagcttcggtctacacattcactgatatgtatacagtggtgagacaggtcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 154 TGCNAAGCTTCTGCTACCTCACCACACTGATGCACTGGGTGAAGAGAGGCTT 213  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 181 ggaagagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggt 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 214 GGACAAAGGCTTGTGATGATGGAATATTAATCATATGATGATGATGATGATGAT 273  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaagaagtgagagagagagcctata 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 274 GAGAAAGTTCAAGACCAAGGCCACATTGACTGTATGATCATCTCCAGCAGCCTACATG 333  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 301 gaacttagttctttagatctgagatacagcgcttatactgtgcaagaagcg----- 354  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 334 CAGCTCAGCAGCCTCACATCTGCGGACTGCTGGGTATATGCTGATCAATAAGTTGCTA 393  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 355 gccctggtatagactactcgtggtggtggtggtggtggtggtggtggtggtggt 405  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 394 CGTTATTCTATGACTGTGGGGTCAAGAACCTCAGTCAAGCCTGCTCTCA 444  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4 819 bp mRNA linear EST 12-JUN-2001  
LOCUS BG966397  
DEFINITION 602832896F1 NCI\_CGAP\_Co24 Mus musculus cdna clone IMAGE:4987631 5',  
mRNA sequence.  
ACCESSION BG966397  
VERSION BG966397.1 GI:14354034  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 819)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

FEATURES  
source Plate: LAM10998 row: O column: 24  
High quality sequence stop: 766.  
Location/Qualifiers  
1..819  
/organism="Mus musculus"  
/strain="FVB/N"

/db\_xref="taxon:10090"  
/clone\_image:4987631  
/clone\_id="NCI\_CGAP\_Co24"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCMV-SpOrf6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 206 a 229 c 199 g 185 t  
ORIGIN

Query Match 58.9%; Score 238.6; DB 10; Length 819;  
Best Local Similarity 75.7%; Pred. No. 1.5e-62;  
Matches 311; Conservative 0; Mismatches 94; Indels 6; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtaccacagctacagtggtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 25 ATGGATGGAGCTGTATCATCTCTCTTTTGTGTACCAACAGCTACAGGTCTCCACTCCAG 84  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 61 gtccagctggtcagctggtggtggtggtggtggtggtggtggtggtggtggtggt 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 85 GTCCAACTGCAGCAGCCTGGGGCTGACCTGGTGAAGCCTGGGACTTCAGTGAAGTTGTCC 144  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 121 tgcnaagcttcggtctacacattcactgatatgtatacagtggtggtggtggtggt 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 145 TGCNAAGCTTCTGCTACCTCACCACACTGATGATGATGATGATGATGATGATGAT 204  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 181 ggaagagcttcggtggtggtggtggtggtggtggtggtggtggtggtggtggt 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 205 GCACAAGCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 264  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaagaagtgagagagagagcctata 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 265 GAGAAAGTTCAAGACCAAGGCCACACTGACTGTAGCAATCCTCCAGCAGCCTACATG 324  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 301 gaacttagttctttagatctgagatacagcgcttatactgtgcaagaagcg----- 354  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 325 CAACTCAGCAGCCTCACATCTGAGGACTGCTGGGTCTATGCTGATGATGATGATGAT 384  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
QY 355 gccctggtatagactactcgtggtggtggtggtggtggtggtggtggtggtggt 405  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 385 TTGCAATGCTATGACTGTGGGGTCAAGAACCTCAGTCAAGCCTGCTCTCA 435  
||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5 770 bp mRNA linear EST 17-JUL-2001  
LOCUS B1249216  
DEFINITION 602994779F1 NCI\_CGAP\_Mam5 Mus musculus cdna clone IMAGE:5150778 5',  
mRNA sequence.  
ACCESSION B1249216  
VERSION B1249216.1 GI:14796364  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 770)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Lothar Hennigshausen Ph.D., Robin Humphreys  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

FEATURES  
source Plate: LAM11372 row: m column: 19  
High quality sequence start: 4  
High quality sequence stop: 769.

FEATURES	Location/Qualifiers
source	1. .770

BASE COUNT	188 a	216 c	193 g	173 t
ORIGIN				

Query Match	58.18;	Score 235.4;	DB 10;	Length 770;
Best Local Similarity	75.28;	Pred. No. 1.4e-61;		
Matches 309;	Conservative 0;	Mismatches 96;	Indels 6;	Gaps 1

OY	1	atgggttggaa	ctgata	ctaa	ctctcttcttcgt	gttaca	agccaa	agggtgtg	caactccag	60
Db	35	atggatggag	gctt	atcatc	ctctcttcttgg	gaagca	acgctt	acagttcc	atccacag	94
OY	61	gtccagctc	gtgtcag	tctctg	ggctag	tgtaag	aaaccc	tggagatc	cagtgaa	120
Db	95	gtccaaact	gtacac	acgctt	ggctgt	gtgctg	cggtga	ggccctg	gaattga	154
OY	121	tgcgaagct	tcgcgct	ctacac	atcact	ctgata	tctgata	cagttgg	tggagagct	180
Db	155	tgcgaagct	cttcgcgct	ctacac	cttccac	acgctt	ctgtgat	ctac	ctggcgga	214
OY	151	ggaacggcc	ctcagat	ggaattg	gagattaa	tattacta	ctatgata	taataca	acatacaac	240
Db	215	gcacaaagg	cccttgat	ggatgttg	gagagat	cttacct	taatag	tatata	ttttaact	274
OY	241	cagaagttc	aaaggc	caagacc	caaatga	ctgtaga	caaatgc	gaagac	caagccata	300
Db	275	gagaagttc	aaaggc	caagacc	caaatga	ctgtaga	caaatgc	ctccag	caacacct	334
OY	301	gaactagtc	ctcttga	gatact	gagata	ctacg	ccgttatt	ctactgt	gtgcaagagcg	355
Db	335	gatctcag	acgctt	gacatct	gagacac	cttgcggg	cttatt	actgtg	ccaagaggg	394
OY	356	-ccigtata	tatg	actact	cgtgggt	ctaaagt	taccct	gtt	taacgctt	405
Db	395	acgttctat	cttgc	atgctgt	ggggcc	acaggg	acac	gctt	acgcttcc	445

[illegible]

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: NCI-CGAP clone distribution  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 plate: LLAM260 row: h column: 21  
 High quality sequence stop: 648.

FEATURES	Location/Qualifiers
source	1. .771

Investigator	providing samples:	Gilbert Smith, NIH
BASE COUNT	179 a	215 c
ORIGIN	195 g	182 t

Query Match	57.7%;	Score 233.8;	DB 10;	Length 771;
Best Local Similarity	73.6%;	Pred. No. 4.3e-61;		
Matches 298; Conservative	0;	Mismatches 107;	Indels 0;	Gaps 0;

QY	1	atgaggttgaaactatatacatctctctctcttggtttaccacaagatcaagagtgctgcaatccag	60
Db	15	atgggaatggggctggggctcttctcttctcttctctgtatgactatgcagaggttcacacagcag	74
QY	61	gtccagctctgctgacagctctggggcttgagggtgaagaagccttgaggatctcagtgaaagtgtcc	120
Db	75	gtttcaggttgaaagcagctatggagctgagctgagctgggtgaaggcttgggggcttcagtgaaagctgccc	134
QY	121	tgcaaagcttcgcgctctacacattcaactctgattatgtctatacagtggtgggtgaagcaggtctcc	180
Db	135	tgcAAGGCTTCCTGGCTTACACCTTCACACAGCATATATTATGCACTGGGTGAACAGAGGGCT	194
QY	181	ggacagggccctcagtgatttgagttatataattctctatgaataatacaactacaac	240
Db	195	ggACAGGGGCTTTGAATGGTATGAGTACTTTTCTCTTTCAAATGATGATACTTAATGCAAT	254
QY	241	cagaagctttaaaggcacaagccacaatgactctagaacaagtcgacagagcacagcctata	300
Db	255	gAGAGTTCAAAGGCAAGGCCACACTGACTGACAGACAAATCCTCCAGCAGACGCCATATG	314
QY	301	gaacttagtctctcttgagatcttgagatacgcgcgtttatctatctgtgcaagagcggcctgg	360
Db	315	GAGCTCAGCAGCCTTACCTCTGAGGACACTGCGCCGCTCTTTACTGTGCAAGGAGGTTACTTAC	374
QY	361	tatatagactactggtgggtcgaaggtacacctgtgacagcgtctccta	405
Db	375	gTATTTGACTACTGGGGCCAAAGCACCACTATACCAAGTCTCTCTCA	419

RESULT	7	
LOCUS	BG669577	
DEFINITION	60283738661 NCI CGAP_kid14 Mus musculus cDNA clone IMAGE:4971813	
	5', mRNA sequence.	

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM0957 row: 1 column: 22  
High quality sequence stop: 723.

FEATURES  
Source  
1. 723  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4971813"  
/lab\_host="NCI\_CGAP\_Kid14"  
/note="Organ: Kidney; Vector: PCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."\*

BASE COUNT 179 a 196 c 193 g 155 t

ORIGIN

Query Match 57.3%; Score 232; DB 10; Length 723;  
Best Local Similarity 74.8%; Pred. No. 1.5e-60;  
Matches 305; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgttaccacagctacaggtgtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 19 ATGGGATGAGAGCTCTATCATCCTCTCTGTGTAGACACAGCTACAGGTGCTCCAG 78  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 gtccagctgtgtcagctctgtgggctcgaagtgaaagcctggagctcagtgaaagtgtcc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 79 GTCCTCACTGAGCAGCCTGGGCTGTGTGTGTGAGCCCTGAGCTCAGTGAAGCTGTGC 138  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 121 tgcgaagcttcgcgctacacatcactcagatgatgtatagtggtgagacagctcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 139 TGCAGAGCTTCTGGCTACACTTACACAGCTACGATGCACTGGGTGAAGCAGAGGCT 198  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 ggacagggcctcgaagtgtgattgagatttaataattactatgataaacactaacac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 199 GGACAAAGCTTGTGATGAGATTGAGAGATTATCTTAATAGTGTAGAGATAACTACAT 258  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 241 cagaagttaaggcgaagccacaaatgactgtagaacagtcgaagcagacagctctatg 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 259 GAGAAAGTTCAAGGGCAAGGCCACACTGACTGTAGACACTCTCCAGCAGAGCTTACGTG 318  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 301 gaacttgcttcttgagatctgagatacgccgtttactatctgtgcaa--gagcgcc 357  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 319 GATCTCAGCAGCCGTGACATCTGAGGACTCTGCGTCTATTCTGTGCAAGAGAGGCCCC 378  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 358 tggatattggaactctgggttcaaggtaccctgttcacccgtctcccta 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 379 AAAGGTTTGTCTACTGGGGCAAGGAGACTGTGCTCACTGCTCTGCA 426  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8  
LOCUS BF168514 724 bp mRNA linear EST 30-OCT-2000  
DEFINITION 601775412F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',  
mRNA sequence.  
ACCESSION BF168514  
VERSION BF168514.1 GI:11048866  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 724)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9265 row: h column: 04  
High quality sequence stop: 661.

FEATURES  
Source  
1. 724  
/organism="Mus musculus"  
/strain="C57BL/6J (F1)"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4017075"  
/lab\_host="NCI\_CGAP\_Lu29"  
/tissue="spontaneous tumor, metastatic to mammary."  
Stem cell origin.  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

BASE COUNT 185 a 186 c 194 g 159 t

ORIGIN

Query Match 57.3%; Score 232; DB 10; Length 724;  
Best Local Similarity 74.8%; Pred. No. 1.5e-60;  
Matches 305; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgttaccacagctacaggtgtgactccag 60  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 38 ATGGGATGAGAGCTCTATCATCCTCTCTGTGTAGACACAGCTACAGGTGCTCCAG 97  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 61 gtccagctgtgtcagctctgtgggctcgaagtgaaagcctggagctcagtgaaagtgtcc 120  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 98 GTCCTCACTGAGCAGCCTGGGCTGTGTGTGTGAGCCCTGAGCTCAGTGAAGTGTGC 157  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 121 tgcgaagcttcgcgctacacatcactcagatgatgtatagtggtgagacagctcct 180  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 158 TGCAGAGCTTCTGGTACTCATCTGCTACACTGCACTGGGTGAAGGAGTCTCT 217  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 181 ggacagggcctcgaagtgtgattgagatttaataattactatgataaacactaacac 240  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 218 GAAAAGAGCTTGTGATGAGATTGAGAGATTATCTTACACTGAGTGTACTACCTAAC 277  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 241 cagaagttaaggcgaagccacaaatgactgtagaacagtcgaagcagacagctctatg 300  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 278 CAGAAAGTTCAAGGGCAAGGCCACACTGACTGTAGCAATCTCCAGCAGAGCTTACATG 337  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 301 gaacttgcttcttgagatctgagatacgccgtttactatctgtgcaa--gagcgcc 357  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 338 CAGCTCAAGAGCCTGACATCTGAGGACTCTGAGTCTATTCTGTGCAAGAGGATCATC 397  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
QY 358 tggatattggaactctgggttcaaggtaccctgttcacccgtctcccta 405  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB 398 AGGCTATGAGACTACTGTGGGTCAAGGAGCTCAGTCAAGCTCTCTCA 445  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9  
LOCUS BF168856 769 bp mRNA linear EST 30-OCT-2000  
DEFINITION 601775314F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:4017147 5',  
mRNA sequence.  
ACCESSION BF168856  
VERSION BF168856.1 GI:11049208  
KEYWORDS EST.

SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS 1 (bases 1 to 769)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LAM9265 row: k column: 04  
High quality sequence stop: 678.  
Location/Qualifiers  
1. 769  
/organism="Mus musculus"  
/strain="C57BL/6J (f1)"  
/db\_xref="taxon:10090"  
/clone\_image="4017147"  
/clone\_lib="NCI-CGAP-Lu29"  
/tissue\_type="spontaneous tumor, metastatic to mammary."  
/stem\_cell\_origin=""  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: Salt; Site\_2: NCI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 190 a 226 c 189 g 164 t  
ORIGIN

Query Match 56.9%; Score 230.4; DB 10; Length 769;  
Best Local Similarity 74.5%; Pred. No. 4.8e-60;  
Matches 304; Conservative 0; Mismatches 101; Indels 3; Gaps 1;

QY 1 atgggttggaactatcatcttcttctgttaccacagctacagtgctacccag 60  
DB 42 ATGGGATGGAGCTGATCTTATTTATCTGTCAGTACAGGCTGCACCTGAG 101  
QY 61 gtccagctgtgctgagctgagctgagaagcctgagctgagctgagctgagctg 120  
DB 102 GTCCAGCTGCAGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 161  
QY 121 tgcgaagcttcggtacacatcactgatacgtacagctgagctgagctgagct 180  
DB 162 TGCAAGGCTTCTGCTACTCATCTGCTACATGCTACATGCTGCTGCTGCTGCT 221  
QY 181 ggaagagggcccgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 240  
DB 222 GAAAGAGAGCTTGTGATGATGAGATGATGATGATGATGATGATGATGATGATG 281  
QY 241 cagaagtttaaggcacaagcacaagcacaagcacaagcacaagcacaagcacaagc 300  
DB 282 CAGAAGTTCAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAG 341  
QY 301 gaacttgcttctgagatctgagatctgagatctgagatctgagatctgagatct 357  
DB 342 CAGCTCAAGAGCTGAGCATCTGAGGACTGCTGAGTCTGATCTGCTGCTGCTGCT 401  
QY 358 tggatatagactactctgagctgagctgagctgagctgagctgagctgagct 405  
DB 402 AGGCTATGAGCTACTGCGGTCAAGGAGCACTCACTCACTCACTCACTCACTCA 449

RESULT 10  
AM403591 488 bp mRNA linear EST 16-FEB-2000  
LOCUS AN403591

DEFINITION UI-HF-BKO-abg-b-01-0-UI.r1 NIH-MGC\_36 Homo sapiens CDNA clone  
IMAGE:3056184 5', mRNA sequence.  
ACCESSION AM403591  
VERSION AM403591.1 GI:6922577  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS 1 (bases 1 to 488)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/biopr/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
1. 488  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="3056184"  
/clone\_lib="NIH-MGC\_36"  
/tissue\_type="lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LRI)"  
/note="Vector: pRT3-Pac; Site\_1: NotI; Site\_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 111 a 136 c 140 g 101 t  
ORIGIN

Query Match 56.0%; Score 226.6; DB 9; Length 488;  
Best Local Similarity 73.5%; Pred. No. 5.8e-59;  
Matches 311; Conservative 0; Mismatches 94; Indels 18; Gaps 1;

QY 1 atgggttggaactatcatcttcttctgttaccacagctacagtgctacccag 60  
DB 2 ACAGAGTGGAGCTGAGGATCTCTTTTGGTGGCAGACGACCAAGTGCCTCCAG 61  
QY 61 gtccagctgtgctgagctgagctgagaagcctgagctgagctgagctgagctgagct 120  
DB 62 GTCCAGCTTGTGATGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 121  
QY 121 tgcgaagcttcggtacacatcactgatacgtacagctgagctgagctgagctgagct 180  
DB 122 TGCAAGGCTTGTGATGATGAGATGATGATGATGATGATGATGATGATGATG 181  
QY 181 ggaagagggcccgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 240  
DB 182 GCACAAAGCTTGTGATGATGAGATGATGATGATGATGATGATGATGATGATG 241  
QY 241 cagaagtttaaggcacaagcacaagcacaagcacaagcacaagcacaagcacaagc 300  
DB 242 CAGAAGTTCAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAGGCGAAG 301  
QY 301 gaacttgcttctgagatctgagatctgagatctgagatctgagatctgagatct 354  
DB 302 GAGCTGAGCAGCTGAGATGATGAGAGCAGCTGATGATGATGATGATGATGATGAT 361  
QY 355 -----gctgtatatagactactgagctgagctgagctgagctgagctgagct 402

DB	364	TACTATGGTTCAGGGAGTTCCTCTTGTACACACTGCGGCGCAGGAGCAACCTCGTACCGTCTCC	421
OY	403	tca 405	111
DB	422	TCA 424	
RESULT	11		
LOCUS	BF580556		
DEFINITION	602097359P1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4217102 5',	764 bp	linear
ACCESSION	BF580556		
VERSION	BF580556.1	GI:11654268	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 764)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaabs-remail.nih.gov		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMN at:		
	http://image.lnl.gov		
	Plate: LAM9795	row: f	column: 15
	High quality sequence stop: 694.		
FEATURES	Location/Qualifiers		
source	1..764		
	/organism="Mus musculus"		
	/strain="FVB/N"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:4217102"		
	/clone_lib="NCI CGAP C024"		
	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: colon; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."		
BASE COUNT	194 a 198 c 195 g 177 t		
ORIGIN			
Query Match	56.0%; Score 226.6; DB 10; Length 764;		
Best Local Similarity	74.1%; Pred. No. 7.le-59;		
Matches	300; Conservative 0; Mismatches 104; Indels 1; Gaps 1;		
OY	1	atgggttggaactgtatcatctcttcttggttaccacagctacaggtgtgcattcccaag 60	
DB	37	ATGGGATGGAGCTCATATCTCTCTTGGTAGACAGCAAGCTACAGGCTCCACCTCCAG 96	
OY	61	gtccagcttggttcacattcggggtcgaagtgaaagaaagctggaggtcagtgaaagtg 120	
DB	97	GTCACACTGCAACACCCCTGGGGTCTTGCTGGCTGGAGCGCTTGACGTTCAGTGAAGCTGTCC 156	
OY	121	tgcagaagcttcgcggtacacattcactgattatgctatcacaagtggtgtagacaagctctc 180	
DB	157	TGCAAGGCTTCTGGCTACACATTCACGACGATCTCGATGACACTGGGTGAAGCAGAGGCTC 216	
OY	181	ggacagggctctcgagtggtatggagttatataattctatgataataacaaatacaaac 240	
DB	217	GGACCAAGGCTTGAATGGA-TGGAGAGAGATTATCTTACTAGTGTGGCAGGACCAACTACAT 275	
OY	241	cagaagtttaaggaggaagggcacaatgactgtgagacaagtcgagagagacagccatata 300	
DB	276	GAGAGCTTCACAGGGGCAAGGCCACACTGACTGTAGACACATCTCTCCAGCAGACCCCTACGCG 335	

QY	301	gaactagttcttcttgaagatcttgaagatacggccgttatttacttgcgaagcggcttg	360
Db	336	GATTTTCACGAGCCTTACATCTGAGGACCTCAGGGGCTCTATTATGTATACAAAGAGGGGAAA	395
QY	361	tatatgagacttggtgtcgaagatgatacccttgcacgccttctca	405
Db	396	GAGTTTGACTACTGGGGCCCAAGGACCACTCTCATATGATCTCTCA	440
RESULT 12			
LOCUS	BC756463	794 bp	RMNA linear EST_15-MAY-2001
DEFINITION	60271579551 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4855894 5',		
ACCESSION	BC756463		
VERSION	BC756463.1	GI:14067116	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 794)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-remail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.nih.gov		
	Plate: L10M1705 row: n column: 23		
	High quality sequence stop: 774.		
FEATURES	Location/Qualifiers		
source	1..794		
	/organism="Homo sapiens"		
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	/clone="IMAGE:4855894"		
	/clone_1db="NIH_MGC_48"		
	/tissue_type="Primary B-cells from tonsils (cell line)"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;		
	Site_2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GCGACGAG(G). Size-selected >500bp		
	for average insert size 1.8kb. Library constructed by Ling		
	Hong in the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: This is a NIH_MGC Library."		
BASE COUNT	173 a 253 c 219 g 149 t		
ORIGIN			
Query Match	55.9%; Score 226.2; DB 10; Length 794;		
Best Local Similarity	73.6%; Pred. No. 9.6e-59;		
Matches 307; Conservative	0; Mismatches 98; Indels 12; Gaps 1;		
QY	1	atgggttggaatgatatcatcttcttcttggttacacagctacagtggtgcacccag	60
Db	47	ATGAGCTGGACCTGGAGAGTCTCTTCTTGGTGGCAGACGACCAAGGCCACATCCAG	106
QY	61	gtccagctgtgtcagctcttggggtcgtgaagaaacctgggagctcagtgaaagtgctc	120
Db	107	GTCGACCTGTGTCAGTCTGGGGCTGAAGAGAGCTGGGGCTCTAGTGAAGGTCTCC	166
QY	121	tgcgaagcttcgcgtgtacacattcactgatatgtatacagtggtgtgaagacgctct	180
Db	167	TGCAGGCTTCTGGATTACCTTCACGCGGCTAATATATGCACTGGGTCGACAGGCCCT	226





QY 1 atgggttgaaactatcatcatctctcttcgtgttaccagaaagctaaagctgtgtaccag 60  
Db 8 ATGGGATGGAGACTGTAATATGCTCTTCTTGGCAGCAAAAGCTACAGGTCTCACATCCAG 67

QY 61 gtccaagctgtgtcagctctgaggcttgaggltgaagaagcctggagctcagtggaagtgctc 120  
Db 68 GTCCAAAGTCAGACAGCCCTGGGGGCTGAGCTTGGAAGCCTGGGGGCTTCAGTAAAGCTGACC 127

QY 121 tgcgaagcttcgcgctaaacatactcaatctatattatgctatacagttggtg-agaacagctcc 179  
Db 128 TGCAAGGCTTGTGGCTACACCTTCACCGTAGTTACTGGATGCACTGGGTAAACCAAGAGGC 187

QY 180 tggagcagggctctgagtgatgtatgaattataataattacatgtgataatacaactacaa 239  
Db 188 TGGACGAGGCGCTTGAGTGATGTGGAAGGATTTGATCTTAATAGTGGTGACTTAAATGACAA 247

QY 240 ccagaagtttaaggaggcacaacatctactgttagacaaagtcagagagacacagcctatat 299  
Db 248 TGAGAAAGTTCAAGAGCAAGGCGACACTGATAGTATGACAAACCCCTCAGACAGGCTTACT 307

QY 300 ggaacttgctcttgagatctgagataagagtcagggcggttattactctgcaagaagcgacctg 359  
Db 308 GCACGCTCAGCAGCCGTGAACATCTGAGAGACTTCGGGCTTATTACTTACAAAGAGAGAGGGGA 367

QY 360 gta-----tatgactactgggtgcagaagctaaccttgtaaccgctctctca 405  
Db 368 TTACGACGCTTATGACATTACTGGGGTCAAGAAACCTCAAGTCAACCGCTCTCTCA 419

RESULT	15
BF165486	
LOCUS	847 bp mRNA linear EST 30-OCT-2000
DEFINITION	B0177739.F1 NCL.CGAP_Lu29 Mus musculus cDNA clone IMAGE:4019039 5' ,
ACCESSION	BF165486
VERSION	BF165486
KEYWORDS	EST .
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Bases 1 to 847)	NIH-MGC	<a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Contact: Robert Strausberg, Ph.D.	Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>	Tissue Procurement: Gilbert Smith, Ph.D.	cdna Library Preparation: Life Technologies, Inc.	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing By: Incyte Genomics, Inc.				
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>				
plate: LLAM9270	row: 1	column: 24	High quality sequence stop: 760.	

## FEATURES

BASE COUNT  
ORIGIN

179 a	223 c	242 g	203 t
-------	-------	-------	-------

Query Match	55.7%;	Score 225.6;	DB 10;	Length 847;
Best Local Similarity	73.8%;	Pred. No. 1.5e-58;		
Matches 301; Conservative	0;	Mismatches 104;	Indels 3;	Gaps 1;

[illegible]

Search completed: August 26, 2002, 16:13:39  
Job time: 4333 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:05:06 ; Search time 266.46 Seconds  
(without alignments)  
2609.586 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
Sequence: 1 atgggttgacgtatcatc.....ccctgtcacccctctccta 405

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :

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24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	405	21	AAA59694
2	334.6	82.6	405	21	AAA59692
3	277.2	68.4	524	12	AAQ14802
4	277.2	68.4	524	12	AAQ14652
5	272.2	67.2	446	11	AAQ05554
6	265.8	65.6	1767	19	AAV61363
7	265.8	65.6	1767	21	AAA78271
8	265.8	65.6	1768	19	AAV61364
9	265.8	65.6	1768	21	AAA78272

10	254.4	62.8	424	17	AAV42717	HuM3 VH coding se
11	253.6	62.6	451	15	AAQ6702	DREB-200 Humanised
12	253.6	62.6	2071	19	AAV70080	Anti-Fas humanised
13	253.6	62.6	2071	21	AAV72184	DNA encoding human
14	253.6	62.6	2071	21	AAV15622	Humanised HFE7A de
15	252	62.2	2073	21	AAV15644	Humanised anti-Fas
16	252	62.2	2073	21	AAV15645	Humanised anti-Fas
17	251.6	62.1	423	21	AAV09905	Humanised antibody
18	250.4	61.8	2073	21	AAV15646	Humanised anti-Fas
19	248.8	61.4	457	19	AAV70104	Humanised anti-Fas
20	248.8	61.4	457	21	AAV72146	Humanised anti-Fas
21	248.8	61.4	457	21	AAV15584	Humanised anti-Fas
22	248.8	61.4	2077	19	AAV70079	Anti-Fas humanised
23	248.8	61.4	2077	21	AAV72159	DNA encoding human
24	248.8	61.4	2077	21	AAV15597	Humanised HFE7A de
25	248.2	61.3	405	21	AAA59698	DNA encoding heavy
26	245.6	60.6	2077	21	AAV15555	Humanised anti-Fas
27	245.2	60.5	423	21	AAV09907	Humanised antibody
28	245	60.5	405	20	AAV33947	Anti-CD33 antibody
29	245	60.5	405	22	AAV58738	Murine M195 antibo
30	245	60.5	411	21	AAA48845	CDNA encoding huma
31	244.8	60.4	409	21	AAZ87738	Anti-human VEGF re
32	244.8	60.4	409	22	AAV70215	CDNA encoding a va
33	243.4	60.1	405	19	AAV37264	Anti-human Flt-1 a
34	243.4	60.1	405	21	AAZ95282	IgM chimeric antib
35	243.4	60.1	1773	18	AAZ88869	H chain subunit of
36	243.4	60.1	1773	19	AAV66735	Anti-human Fas mon
37	243.4	60.1	1773	21	AAV78202	Anti-human Fas ant
38	242.2	59.8	478	20	AAV88433	EST clone GF196.
39	241.8	59.7	433	13	AAQ24790	Anti-Fas antibody
40	240.8	59.5	421	18	AAV73624	CDNA for humanised
41	240.2	59.3	443	10	AAV91620	DNA sequence of th
42	240	59.3	409	21	AAZ87778	Anti-human VEGF re
43	240	59.3	409	22	AAV70251	Anti-human Flt-1 a
44	239	59.0	418	19	AAV59116	HML.24 antibody he
45	239	59.0	418	19	AAV07581	Anti-human HML.24

#### ALIGNMENTS

RESULT	1
AAA59694	standard; DNA: 405 BP.
ID	AAA59694
AC	AAA59694;
XX	
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding heavy chain variable region of humanised 3S1 antibody.
XX	
DE	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
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FT	/*tag= a
FT	/product= "heavy chain variable region of 3D1 antibody"
FT	/note= "no termination codon given"
FT	sig_peptide 1..57
FT	/*tag= b
FT	mat_peptide 58..405
FT	/*tag= c
XX	
XX	

PN WO200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 XX 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;  
 XX  
 DR WPI: 2000-524532/47.  
 DR P-PSDB; AAB07965.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 XX  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC humanised murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulin, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 405 BP; 102 A; 88 C; 110 G; 105 T; 0 other;

Query Match 100.0%; Score 405; DB 21; Length 405;  
 Best Local Similarity 100.0%; Pred. No. 1e-101;  
 Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgggttgagactgtacatctcttctgtgtacacagctacaggtgtgacccag 60  
 |||||||  
 DB 1 atgggttgagactgtacatctcttctgtgtacacagctacaggtgtgacccag 60  
 QY 61 gtccagctgtgtcagctctgtgggtgaagtgaaagccttggaagctcagtgaaagtcc 120  
 |||||||  
 DB 61 gtccagctgtgtcagctctgtgggtgaagtgaaagccttggaagctcagtgaaagtcc 120  
 QY 121 tgcgaagcttcggtcaccatctacatctgattatgtctatagctgtggagacagagccct 180  
 |||||||  
 DB 121 tgcgaagcttcggtcaccatctacatctgattatgtctatagctgtggagacagagccct 180  
 QY 181 ggcacagagcctcagtgatgtgattatcaataattacatagataataacaatacaac 240  
 |||||||  
 DB 181 ggcacagagcctcagtgatgtgattatcaataattacatagataataacaatacaac 240  
 QY 241 cagaagtttaaggcgaagccacaatgactgtagacaaagctgcagacagacagctatag 300  
 |||||||  
 DB 241 cagaagtttaaggcgaagccacaatgactgtagacaaagctgcagacagacagctatag 300  
 QY 301 gaatttgtcttgaatctgagataagcgcggttatactacgtgcagaagcggtctgg 360  
 |||||||  
 DB 301 gaatttgtcttgaatctgagataagcgcggttatactacgtgcagaagcggtctgg 360  
 QY 361 tatactgactacgtgggttcaaggtacacctgttcacgctccctca 405  
 |||||||  
 DB 361 tatactgactacgtgggttcaaggtacacctgttcacgctccctca 405

RESULT 2  
 AAA59692  
 ID AAA59692 standard; DNA; 405 BP.  
 XX  
 AC AAA59692;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Nucleotide sequence of heavy chain variable region of 3S1 antibody.  
 XX  
 XX Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;  
 KW autoimmune disease; infectious diseases; inflammatory disorder;  
 KW systemic lupus erythematosus; diabetes mellitus; insulin; asthma;  
 KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;  
 KW multiple sclerosis; transplant rejection; proliferative disease;  
 KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KW aplastic anaemia; myeloid dysplasia syndrome; ss.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..405  
 FT /tag- a  
 FT /product= "heavy chain variable region of 3D1 antibody"  
 FT /note= "no termination codon given"  
 FT sig-peptide 1..57  
 FT /tag- b  
 FT mat-peptide 58..405  
 FT /tag- c  
 XX  
 PN WO200047625-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 09-FEB-2000; 2000MO-US03303.  
 XX  
 PR 12-FEB-1999; 99US-0249011.  
 XX 24-JUN-1999; 99US-0339596.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 XX Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GW;  
 XX  
 DR WPI: 2000-524532/47.  
 DR P-PSDB; AAB07963.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 XX  
 PS Example 1; Fig 1A; 162pp; English.  
 XX  
 CC The present sequence encodes the heavy chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulin, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX  
 SQ Sequence 405 BP; 110 A; 89 C; 102 G; 104 T; 0 other;



Pf	XX
Pf	29 -APR-1991; 91WO-US02946.
PR	XX
PR	27 -APR-1990; 90GB-0009548.
XX	XX
PA	(CELL-) CELLTECH LTD.
XX	(BOEH ) BOEHRINGER INGELHEIM PHA.
PI	Adelr JR, Robinson MK, Bright SM, Roehlein RA;
XX	WPI: 1991-353534/48.
DR	P-PSDB; AARI5200.
XX	XX
PT	New humanised chimeric anti-ICAM-1 antibodies - useful in
PT	treating inflammation e.g. psoriasis and ulcerative colitis to
PT	suppress metastasis of haematopoietic tumour cell and in
PT	diagnosis.
XX	XX
PS	Claim 10; Fig 2; 85pp; English.
XX	XX
CC	The sequence comprises the 5' untranslated region, signal sequence,
CC	variable region and part of the constant region for the R6-5-6D
CC	murine Mab heavy chain. The hybridoma cell line R6-5-D6 producing
CC	the anti ICAM-1 Ab was provided by Boehringer Ingelheim
CC	Pharmaceuticals Inc. The cells were grown and mRNA isolated and
CC	used to prepare cDNA for a library in pSP64 vector DNA. The
CC	library was grown in E. coli LM1035 and colonies screened using a
CC	probe complementary to a sequence in the mouse kappa constant
CC	region or with a 980 bp BamHI-EcoRI restriction fragment of a
CC	previously isolated mouse IgG2a constant region clone. Ten
CC	positive clones were isolated and rescreened. Positive clones from
CC	the second round of screening were grown and the DNA inserts
CC	sequenced. The DNA was used to construct a humanised Abs having
CC	chimeric variable regions, esp. with IgG human constant region
CC	domains. The Abs can be used to treat inflammation, to suppress
CC	metastasis of haematopoietic tumour cells and growth of ICAM-1
CC	expressing tumour cells, to treat viral infection, to suppress
CC	extravasular migration of virally infected leucocytes and to treat
CC	asthma.
CC	See also AAQ14651 and AAQ14830.
XX	XX
SQ	Sequence 524 BP; 128 A; 130 C; 135 G; 131 T; 0 other;
XX	XX
Query Match	68.4%; Score 277.2; DB:12; Length 524;
Best Local Similarity	81.4%; Pred. No. 1.4e-66;
Matches 337; Conservative	0; Mismatches 68; Indels 9; Gaps
OY	1 atgggttggaactgcatcattcttcttcgcgtgtaccacagcgtacaggtgtgacctccag 60
Db	34 atgggttgaggatgatcaattcttcttcgtgtgagaacaacgctaacagggtgtgacctccag 93
OY	61 gtccagctcggtgcagtctcggtggcgtgaagtgaaagccttggagctcagttgaagtgtcc 120
Db	94 gtccagcgtcgagcagatctcgtgcttagcgtcggtgaaggccttggatcctcagtagaatccc 153
OY	121 tgcgaagcttcgggtgtatacattcacctgatatgttatatacagttgggttggaaagcttct 180
Db	154 tgcgaaggtcttcgggtgtacacattcattcttgtcattacacactgggtgtgaaggagatcat 213
OY	181 ggcacagggcctcagatctgagtttgagtttaataatctaactgaataataacaactacaac 240
Db	214 gcaaaagctctcagatctgagtttgagtttaatttgcttactctgtgacacaacaactacaac 273
OY	241 cagaagtttaagggtgaagggcccaatgactgtgagacaagtgcagcagcagcattatag 300
Db	274 cagaagtttaagggtgaagggcccaatgactgtgacaaaactcctccaacacagcattatg 333
OY	301g gaactagttctcttgaggatctgagatacgcggctttattactgtgcgaagcggtcg 360
Db	334 ggaactgtccagatctgacatctgagatcttcgccactatattactgtgcgaagagggatg 393
OY	361 -----tatatgactactgggttcaaggtlacccttgtltaacggtctctca 405

[illegible]

Dd	285	cgaggggtttaaggcgaagccacaatgactgtagtgaacaacatcctccaagcacagcctaattg	344
Oy	301	gaacttaagtcttttgagatctgtagatacggcgttattactgtgtcaagaagcgacctg	360
Dd	345	gaacttcgcagatgatgactctgcgaatcttcgcatactatctgtgtcaaaa---ggaagc	401
Oy	361	tatatgactactgtggtgtcaagtgaccctgtgtaaccgtgcccca	405
Dd	402	aaccttgactactgtggccaaagccaccactctcacagttcccctca	446
RESULT	6	:	:
AAV61363	standard; cDNA to mRNA; 1767 BP.	:	:
AC	AAV61363;	:	:
Dt	18-JAN-1999 (first entry)	:	:
De	Anti-human Fas humanised antibody CH11 heavy chain Hmuh cDNA.	:	:
Kw	Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;	:	:
Kw	autoimmune disease; rheumatoid arthritis; therapy; human;	:	:
Xx	antibody engineering; ds.	:	:
Os	Homo sapiens.	:	:
Os	Synthetic.	:	:
Ff	Key	Location/Qualifiers	
Ff	s1g_peptide	1..57	
Ff	/+tag-	a	
Ff	mat_peptide	58..1764	
Ff	/+tag-	b	
Pn	EP866131-A2.		
Xx			
Xx	23-SEP-1998.		
Pd			
Xx	20-MAR-1998; 98EP-0302113.		
Pf			
Xx	21-MAR-1997; 97JP-0067938.		
Pr			
Xx	(SANY ) SANKYO CO LTD.		
Pa			
Pl	Haruyama H, Nakahara K, Serizawa N, Takahashi T,		
Pl	Yonehara S;		
Xx			
Dr	WPI: 1998-482965/42.		
Dr	P-PSDB; AAW71880.		
Xx			
Pt	Production of anti-Fas protein humanised antibodies - for use in		
Pt	inducing apoptosis on Fas expressing cells in the treatment of		
Pt	autoimmune diseases, especially rheumatoid arthritis		
Xx			
Ps	Example 3; Page 103-105; 187pp; English.		
Cc	This CDNA sequence codes for a humanised anti-Fas antibody CH11		
Cc	heavy chain (see AAW71880), designated Hmuh. Hmuh is based on the		
Cc	light chain (see AAW71880) of murine anti-human Fas monoclonal		
Cc	antibody CH11. The humanised sequence was designed following		
Cc	selection of donor residues from CH11 to be grafted onto acceptor		
Cc	molecule 21.28/CL. 2 light chain sequences (see AAW71880-81) have		
Cc	been designed, and each can be used in combination with any of 4		
Cc	light chain sequences (see AAW71876-79) to provide novel, claimed		
Cc	humanised CH11 IgM antibodies that lack a J' chain. These humanised		
Cc	anti-human Fas antibodies are capable of inducing apoptosis in cells		
Cc	expressing Fas (e.g. synovialocytes) and are useful in the treatment		
Cc	of autoimmune disease and chronic rheumatoid arthritis. DNA		
Cc	sequences encoding the humanised antibodies are claimed, as are		
Cc	vectors such as pRmuH5-1 including the Hmuh nucleotide sequence,		
Cc	and host cells such as Escherichia coli pRmuH5-1 (FERM BP--5863).		
Xq	Sequence 1767 BP; 384 A; 568 C; 485 G; 330 T; 0 other;		

Query Match	Similarity	78.5%	Pred. No. 2.5e-63	DB 19	Length 1767
Best Local	Similarity	78.5%	Pred. No. 2.5e-63	DB 19	Length 1767
Matches	318	Conservative	0	Mismatches	87
				Indels	0
				Gaps	0
QY	1	atgggttggaactgtatcatctctcttcttggttaccacagctacagatgtgcaactccag	60		
Db	1	atgggattgagcttgatct	60		
QY	61	gtccagctgtgctgcaagctctggggcttgaggttgaagaagcctggagctcagttgaagtgctc	120		
Db	61	gtccagctgtgctgcaagctctggggcttgaggttgaagaagcctggagctcagttgaagtgctc	120		
QY	121	tgcgaagctctccgggtacacatctctatctgtatctgtatcagttggttgagcaagctctct	180		
Db	121	tgcgaagctctccgggtacacatctctatctgtatctgtatcagttggttgagcaagctctct	180		
QY	181	ggacagagggcctccagctgagatttgagatttaataattactatgataatacaaacatacaac	240		
Db	181	ggacagagggcctccagctgagatttgagatttaataattactatgataatacaaacatacaac	240		
QY	241	cagaaagtttaaggaggaagcccaatgactgtagcaagctcgacagacagacgtctatgt	300		
Db	241	cagaaagtttaaggaggaagcccaatgactgtagcaagctcgacagacagacgtctatgt	300		
QY	301	gaactatgtctcttgagattctgagatacggcgcgttttactgtgcaagcgcgctcgtg	360		
Db	301	gaactatgtctcttgagattctgagatacggcgcgttttactgtgcaagcgcgctcgtg	360		
QY	361	tatatgactactgggggtcgaaggtacacctgtgacacctctccca	405		
Db	361	gctatgactactgggggtcgaaggtacacctgtgacacctctccca	405		
RESULT	7				
AAA78271					
ID	AAA78271	standard; DNA; 1767 BP.			
XX	AAA78271;				
AC					
XX					
DT	16-NOV-2000	(first entry)			
XX					
DE	Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #85.				
XX					
KW	Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;				
KW	immunosuppression; autoimmune disease; treatment; rheumatism;				
KW	anti-Fas antibody; ss.				
XX					
OS	Synthetic.				
XX					
PN	JP2000154149-A.				
XX					
PD	06-JUN-2000.				
XX					
PF	17-SEP-1999; 99JP-0263984.				
XX					
PR	18-SEP-1998; 98JP-0264598.				
XX					
PA	(SANYO ) SANKYO CO LTD.				
XX					
DR	WPI: 2000-454476/40.				
XX					
P	P-PSDB: AAB12917.				
XX					
PT	Anti-human Fas humanizing antibody-containing antirheumatic agents				
XX					
PS	Example 2; Page 73-75; 109pp; Japanese.				
XX					
CC	The present invention relates to antirheumatic agents which comprise as				
CC	active ingredients an immunoglobulin M (IgM) protein. The IgM protein				
CC	does not include a J segment, has apoptosis inducing activity, and				
CC	consists of a light and heavy chain polypeptide produced synthetically.				
CC	The agents of the invention exhibit antirheumatic and immunosuppressive				

CC activity and can be used to treat autoimmune diseases, especially  
 CC rheumatism. The IgM molecule used in the invention are nucleotide sequences  
 CC binding properties. Included in the invention are nucleotide sequences  
 CC of the IgM light and heavy chains (see AA878267-A78272) and the  
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see  
 CC AA878202-A78206) and protein sequences (see AAB12908-B12910). Also  
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
 CC chains used in the invention are represented by sequences  
 CC AA878213-A78266. Primers used for sequencing the human Ig DNA used in the  
 CC invention are represented by sequences AA878277-A78318 and  
 CC AA878335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
 CC represented by sequences AA878321-A78334 and AA878338-A78367. Primer  
 CC sequences AA878207-A78212 are specific for murine Ig DNA, and are used in  
 CC the production of the agent of the invention.  
 XX  
 SQ Sequence 1767 BP; 384 A; 568 C; 485 G; 330 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1767;  
 Best Local Similarity 78.5%; Pred. No. 2.5e-63;  
 Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttcttggttacccagcagcaggtgtcacctccag 60  
 DB 1 atgggattgagcgtcgtctcttctctctctccctcaggaactcagcgtccactctgag 60  
 QY 61 gtccacgtgtgtgagctgtggtgtggaagaacccgtggagcctcagtgaaagtgtcc 120  
 DB 61 gtgcagctctgtgagctgtggtgtggaagaacccgtggagcctcagtgaaagtgtcc 120  
 QY 121 tggaaagcttcggcgtccacatcgtatgtatcgtacagtggtgtgaaagcgtctcc 180  
 DB 121 tggaaagcttcgtgatacacctcactgactacataatgcatgtgtgtgtgtgtgtgtcc 180  
 QY 181 ggaacagggcctcgtgagttgagttatgaattactatgaataataacaatacaac 240  
 DB 181 ggaacagggcctcgtgagttgagttatgaattactatgaataataacaatacaac 240  
 QY 241 cagaagttaaggcagaagccacaatgactgtgacaagtcgagcagcagcagcctatg 300  
 DB 241 cagaagttaaggcagaagccacaatgactgtgacaagtcgagcagcagcagcctatg 300  
 QY 301 gaactagttcttcttgagatcgtgagtaacggtttattactgttcaagaagcgtctg 360  
 DB 301 gaactagttcttcttgagatcgtgagtaacggtttattactgttcaagaagcgtctg 360  
 QY 361 tataatgactcgtgggtcagaagttaccctgttcaacgctctccta 405  
 DB 361 gcatgtgactactgtggcaggaaccctgtgtacacgtctctcca 405

RESULT 8

AA61364  
 ID AA61364 standard; cDNA to mRNA; 1768 BP.

AA61364;

18-JAN-1999 (first entry)

DE Anti-human Fas humanised antibody CH11 heavy chain HmuM cDNA.

XX Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

XX antibody engineering; ds.

XX Homo sapiens.

XX Synthetic.

FT Key Location/Qualifiers  
 CDS 1..1767  
 FT /tag= a

FT sig\_peptide 1..57  
 FT /tag= b  
 FT mat\_peptide 58..1764  
 FT /tag= c  
 XX EP866131-A2.  
 XX 23-SEP-1998.  
 XX 20-MAR-1998; 98EP-0302113.  
 XX 21-MAR-1997; 97JP-0067938.  
 XX (SANY ) SANKYO CO LTD.  
 XX Haruyama H, Nakahara K, Serizawa N, Takahashi T;  
 PI Yonehara S;  
 DR WPI; 1998-482965/42.  
 DR P-PSDB; AAW71881  
 XX  
 PT Production of anti-Fas protein humanised antibodies - for use in  
 PT inducing apoptosis on Fas expressing cells in the treatment of  
 PT autoimmune diseases, especially rheumatoid arthritis  
 XX  
 XX Example 3; Page 108-110; 187Pp; English.

CC This cDNA sequence codes for a humanised anti-Fas antibody CH11  
 CC heavy chain (see AAW71881), designated HmuM. HmuM is based on the  
 CC light chain (see AAW71888) of murine anti-human Fas monoclonal  
 CC antibody CH11. The humanised sequence was designed following  
 CC selection of donor residues from CH11 to be grafted onto acceptor  
 CC molecule 21.28/CL. 2 light chain sequences (see AAW71880-81) have  
 CC been designed, and each can be used in combination with any of 4  
 CC light chain sequences (see AAW71876-79) to provide novel, claimed  
 CC humanised CH11 IgM antibodies that lack a J chain. These humanised  
 CC anti-human Fas antibodies are capable of inducing apoptosis in cells  
 CC expressing Fas (e.g. synovialocytes) and are useful in the treatment  
 CC of autoimmune disease and chronic rheumatoid arthritis. DNA  
 CC sequences encoding the humanised antibodies are claimed, as are  
 CC vectors such as pMmuM-1 including the HmuM nucleotide sequence,  
 CC and host cells such as Escherichia coli pMmuM1-1 (FERM BP-5864).  
 XX  
 SQ Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 19; Length 1768;  
 Best Local Similarity 78.5%; Pred. No. 2.5e-63;  
 Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctcttcttggttacccagcagcaggtgtcacctccag 60  
 DB 1 atgggattgagcgtcgtctcttctctctctccctcaggaactcagcgtccactctgag 60  
 QY 61 gtccacgtgtgtgagctgtggtgtggaagaacccgtggagcctcagtgaaagtgtcc 120  
 DB 61 gtgcagctctgtgagctgtggtgtggaagaacccgtggagcctcagtgaaagtgtcc 120  
 QY 121 tggaaagcttcggcgtccacatcgtatgtatcgtacagtggtgtgaaagcgtctcc 180  
 DB 121 tggaaagcttcgtgatacacctcactgactacataatgcatgtgtgtgtgtgtgtgtcc 180  
 QY 181 ggaacagggcctcgtgagttgagttatgaattactatgaataataacaatacaac 240  
 DB 181 ggaacagggcctcgtgagttgagttatgaattactatgaataataacaatacaac 240  
 QY 241 cagaagttaaggcagaagccacaatgactgtgacaagtcgagcagcagcagcctatg 300  
 DB 241 cagaagttaaggcagaagccacaatgactgtgacaagtcgagcagcagcagcctatg 300  
 QY 301 gaactagttcttcttgagatcgtgagtaacggtttattactgttcaagaagcgtctg 360  
 DB 301 gaactagttcttcttgagatcgtgagtaacggtttattactgttcaagaagcgtctg 360



QY 361 tatatgactactggtggtcaaggtaccctgtcaccgtctccctca 405  
|||||  
Db 361 gcatggtactactggtggcgaaggaacctgtgtcaaccgtctccctca 405

RESULT 9  
AAA78272  
ID AAA78272 standard; DNA: 1768 BP.  
AC AAA78272:  
XX 16-NOV-2000 (first entry)  
DT  
DE Anti-human Fas immunoglobulin M heavy chain DNA sequence SEQ ID #87.  
XX  
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;  
KM immunosuppression; autoimmune disease; treatment; rheumatism;  
KW anti-Fas antibody; ss.  
XX  
XX Synthetic.  
OS  
PN JP2000154149-A.  
PD 06-JUN-2000.  
PF 17-SEP-1999; 99JP-0263984.  
PR 18-SEP-1998; 98JP-0264598.  
XX  
XX (SANY ) SANKYO CO LTD.  
PA WPI: 2000-454476/40.  
DR P-PSDB; AAB12918.  
XX  
XX Anti-human Fas humanizing antibody-containing antirheumatic agents -  
PT Example 2; Page 77-79; 109pp; Japanese.  
PS  
XX The present invention relates to antirheumatic agents which comprise as  
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein  
CC does not include a J segment, has apoptosis inducing activity, and  
CC consists of a light and heavy chain polypeptide produced synthetically.  
CC The agents of the invention exhibit antirheumatic and immunosuppressive  
CC activity and can be used to treat autoimmune diseases, especially  
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen  
CC binding properties. Included in the invention are nucleotide sequences  
CC of the IgM light and heavy chains (see AAA78267-A78272) and the  
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and  
CC nucleotide sequences of the humanised anti-human Fas Ig CH1 (see  
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also  
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).  
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa  
CC chains used in the invention are represented by sequences  
CC AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the  
CC invention are represented by sequences AAA78277-A78318 and  
CC AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are  
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer  
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in  
CC the production of the agent of the invention.  
XX  
XX Sequence 1768 BP; 387 A; 564 C; 485 G; 332 T; 0 other;

Query Match 65.6%; Score 265.8; DB 21; Length 1768;  
Best Local Similarity 78.5%; Pred. No. 2, 5e-63;  
Matches 318; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatctctcttctgtgtaccacaggtacaggtgacatccacg 60  
|||||  
Db 1 atgggttggaactgtatctctctctctctctctgtcagaactgcaggtgcacactctgag 60  
61 gtccagctgtgtcagctctgtggtcgtgaggtgaagaagccttggagctcagtgaaagtgtcc 120

Db 61 gtgcagcttgtgcagctctggtggcaggtggaagacctgggacctcagtgaaagtttcc 120  
QY 121 tgcagaacctccggctacacattacatgatatgtctacagtggtggaagacctccct 180  
|||||  
Db 121 tgcagaacctcttgatcacaccttcacataataatgctgtggtggaagacctccat 180  
QY 181 ggcagaagcctcagatgtgatgtgattataataattactactgataataacataaac 240  
|||||  
Db 181 ggaagaagcctcagatgtgatgtgattataataattactactgataataacataaac 240  
QY 241 cagaatttaagggcagaagccacaaatgactgtagacaagtcgaagcagacagctata 300  
|||||  
Db 241 cagaagttcaagcagaagccacaaatgactgttagacaattccgcgacagacagctatg 300  
QY 301 gaacttagctcttgaagatcctggaagatcagcagcgtttactactgtgcaagagcgctg 360  
|||||  
Db 301 gactgtgacagcctggaagatcctggaagacagcgtgtgtattactgtgcgagaagttactat 360  
QY 361 tatatgactactggtggtcaaggtaccctgtcaccgtctccctca 405  
|||||  
Db 361 gcatggtactactggtggcgaaggaacctgtgtcaaccgtctccctca 405

RESULT 10  
AAT42717  
ID AAT42717 standard; DNA: 424 BP.  
XX  
XX AAT42717:  
AC  
XX  
XX 04-FEB-1997 (first entry)  
DT  
DE HUMC3 VH coding sequence.  
XX  
XX Humanised antibody; variable heavy region; buried residue modification;  
KM VH: HUMC3 VH: BA46 antigen; human; milk fat globule; HMG; lactation;  
KW fat globule membrane; murine; mammary epithelial cell; breast cancer;  
KM breast membrane glycoprotein; therapy; immunotherapy; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX Key Location/Qualifiers  
FH 11.418  
FT /\*tag- a  
FT CDS /product= HUMC3 VH (BR-M version)  
PN MO9608565-A2.  
XX  
PD 21-MAR-1996.  
XX  
XX 14-SEP-1995; 95WO-US11683.  
PF  
XX 07-JUN-1995; 95US-0487598.  
PR 16-SEP-1994; 94US-0307868.  
XX  
XX (CANC-) CANCER RES FUND CONTRA COSTA.  
PA  
XX Certani RI, Do Couto FJR, Peterson JA;  
PI WPI: 1996-179941/18.  
DR P-PSDB; AAM06442.  
XX  
XX Recombinant Mc3 antibody which binds BA46 antigen of HMG -  
PT comprises a modified heavy or light chain variable region, useful in  
DT the diagnosis and therapy of breast cancer  
XX  
PS Claim 13; Fig 18; 91pp; English.  
XX  
XX This sequence represents the coding sequence for the variable heavy (VH)  
CC chain of the humanised murine antibody HUMC3 VH. The Mc3 VH sequence was  
CC humanised using the buried residue modification technique, where  
CC important non-human framework residues are unaffected. The Mc3 antibody  
CC binds to the BA46 antigen of the human milk fat globule (HMG). The milk

CC fat globule membrane is derived from the apical surface of the mammalian  
CC epithelial cell during lactation, and therefore is a source for breast  
CC membrane glycoproteins. The antibody can be used in an in vitro method  
CC to detect a HMG antigen (or antigen fragment), and to diagnose the  
CC presence of the antigen in a subject. The antibody can also be used to  
CC deliver an agent to a target (within a subjects body), containing a HMG  
CC antigen. The antibodies can also be used for diagnosis, prognosis, and  
CC therapeutic applications of breast cancer. As the humanised antibodies  
CC retain their high affinity binding to the antigen, they are useful for  
CC immunodiagnostic and immunotherapeutic applications in humans.  
XX  
SQ Sequence 424 BP; 106 A; 102 C; 112 G; 104 T; 0 other;

Query Match 62.8%; Score 254.4; DB 17; Length 424;  
Best Local Similarity 78.2%; Pred. No. 2.3e-60;  
Matches 319; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgcaactccag 60  
DB 11 atgaaatgacgtctgtgtatctctctctctctgtcagaactgtcagctcactctgag 70  
QY 61 gtccagctgtgtcagctctgtggtcgaagtgaagaagcctgtgagctcagtgatgtcc 120  
DB 71 gtccagctgtgtcagctctgtggtcgaagtgaagaagcctgtgagctcagtgatgtcc 130  
QY 121 tgcagaagcttcgcgcctacacattactcagtgatgatacagtggtgtgagcagctctc 180  
DB 131 tgcagaagcttcgtttactacatcaccagctacacagcctgtgtgaaagcagacct 190  
QY 181 ggaacaggcctcgtggtgtggtgtggtatataatattactatgataataacaactaac 240  
DB 191 ggaatgaacctgtggtgtggtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 250  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaacaagtgcagagacagctctatgt 300  
DB 251 cagaagttccaggaacagccacaaatgactgtagaacaagtgcagagacagctctatgt 310  
QY 301 gaacttagcttcgtgagctcgaagatagcgccttatactgtgcaagagcgccctgtg 360  
DB 311 gagctcagcagctcgtgagctcgaagatagcgccttatactgtgcaagagcgccctgtg 370  
QY 361 ta---tatgactactcgtggtcgaaggtacacctgtcacgcgtctccca 405  
DB 371 tatactatgactatgtggtgcaaggaacctgtgcacctctctca 418

## RESULT 11

AA066702 standard; cDNA; 451 BP.

XX  
AC AA066702;  
XX  
DT 16-NOV-1994 (first entry)  
XX  
DE DREG-200 Humanized antibody heavy chain variable region.  
XX  
KW DREG-200; L-selectin; LECAM-1; Mel-14; LAM-1;  
KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;  
KW complementarity determining region; CDR; monoclonal antibody; Mab;  
KW framework; light chain; heavy chain; variable domain;  
KW monoclonal antibody; acceptor antibody Eu; transgenic animal; ss.  
XX  
OS Mus sp.; Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 12..434  
FT /\*tag= a  
FT sig\_peptide 12..68  
FT /\*tag= b  
FT mat\_peptide 69..431  
FT /\*\*tag= c  
XX

PN W09412215-A.  
XX 09-JUN-1994.  
XX 30-NOV-1993; 93WO-0511612.  
XX 01-DEC-1992; 92US-0983946.  
XX (PROT-) PROTEIN DESIGN LABS INC.  
XX Co MS;  
XX WPI: 1994-199974/24.  
XX P-PSDB; AAR55556.  
XX  
XX New humanised antibody specific for L-selectin - with murine CDR  
XX and human framework regions, inhibits binding of neutrophils to  
XX endothelial cells and useful for treating or preventing  
XX inflammation  
XX  
XX Disclosure; Fig. 3B; 60pp; English.

CC An L-selectin-specific IgG1 or IgG4 humanized antibody has CDRs  
CC corresponding to those of mouse Mab DREG-200 and heavy and light  
CC chain variable region frameworks of the human acceptor antibody Eu.  
CC Nucleotide and aa sequences are provided for the DREG-200 light  
CC (AA066699, AAR55553) and heavy (AA066700, AAR55554) chain variable  
CC regions and the humanized DREG-200 light (AA066701, AAR55555) and heavy  
CC (AA066702, AAR55556) chain variable regions. The humanized antibodies  
CC can be produced economically in large quantities by expression in  
CC mammalian cell culture or in transgenic animals.  
XX  
SQ Sequence 451 BP; 120 A; 105 C; 116 G; 110 T; 0 other;

Query Match 62.6%; Score 253.6; DB 15; Length 451;  
Best Local Similarity 77.6%; Pred. No. 4e-60;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

QY 1 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgcaactccag 60  
DB 12 atgggttggaactgtatcatcttcttctgtgtacacagctacaggtgtgcaactccag 71  
QY 61 gtccagctgtgtcagctctgtggtcgaagtgaagaagcctgtgagctcagtgatgtcc 120  
DB 72 gtccagctgtgtcagctctgtggtcgaagtgaagaagcctgtgagctcagtgatgtcc 131  
QY 121 tgcagaagcttcgcgcctacacattactcagtgatgatacagtggtgtgagcagacct 180  
DB 132 tgcagaagcttcgtatcacatcactcagtgatgtatgacactgtgtgtgagcagacct 191  
QY 181 ggaacaggcctcgtggtgtggtgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240  
DB 192 ggtcaagcagctcgt 251  
QY 241 cagaagtttaaggcgaagccacaaatgactgtagaacaagtgcagagacagctctatgt 300  
DB 252 gagaagtttcaaggcgaagccacaaatgactgtagaacaagtgcagagacagctctatgt 311  
QY 301 gaacttagcttcgtgagctcgaagatagcgccttatactgtgcaagagcgccct-- 358  
DB 312 gaactcagcagctcgtgagctcgaagatagcgccttatactgtgcaagagcgccct 371  
QY 359 -----ggtatagactactcgtggtcgaaggttacacctgtcacgcgtctccca 405  
DB 372 ggtactacagctcgtgtactcgtatgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 431

## RESULT 12

AAV70080  
ID AAV70080 standard; DNA; 2071 BP.  
XX  
AC AAV70080;



KW murine:humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; heavy chain; ds.  
 XX  
 XX Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 XX JP2000163933-A.  
 PN  
 PD 20-JUN-2000.  
 PF  
 XX 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 XX WPI; 2000-485645/43.  
 DR P-PSDB; AAB14779.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 PT  
 PS Example 22; Page 106-108; 139pp; Japanese.  
 XX  
 CC The invention relates to compositions for the prevention or treatment  
 CC of diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAA72146, AAA72159, and AAA72164  
 CC represent DNA encoding the heavy chains (or fragments thereof) of  
 CC various humanised HFE7A-derived anti-Fas antibodies.  
 XX  
 XX Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match	62.6%	Score 253.6	DB 21	Length 2071
Best Local Similarity	77.6%	Pred. No. 5.9e-60		
Matches 326	Conservative 0	Mismatches 79	Indels 15	Gaps 1
QY 1	atgggtctggaactgcatcatctctcttcctggtgtaccacagctacaggtgtgcactcccaag	60		
Db 21	atgggatctgagctcgtatcatctctctctctcttcttgtagaacaacagctacaggtgtccactctcaag	80		
QY 61	gtccagctctgtctgcagctctctggtgctgaagctbgaagaagcctbgtgagctcagctgaagctgtcc	120		
Db 81	gtccacactctgtctgcagctctctggtgctgaagctbgaagaagcctbgtgagctcagctgaagctgtcc	140		
QY 121	tgcgaagcttcctgcgtatacaatctacatgataatgtctatacagctggtgtgaagaagctcct	180		
Db 141	tgcgaagctctctctgcgtatacaatctccacagctctctgtgaatgtggtgtgaataaagctccct	200		
QY 181	ggacagagcctccagctgagctatggaatttaatacttaactaactgataataacaacacacac	240		
Db 201	ggacagagcctcttgagctggaatggtggaagaagcttgatcctctctgataagctataactataccaat	260		
QY 241	cagaaagtttaaggggcgaagccacaacatgactctlagaacaagctgcagcagacagacgtatag	300		
Db 261	caaaagcttcaaggggaagggccaacatctgactctgtagacacataccacatcagcacagcctcaatg	320		
QY 301	gaactagttctcttgagatctcgaagatacagcgcttatactactcgtgcaaga-----	351		
Db 321	gagctccagcagacgtatgagctctgtagagacacagcgggtgctcttactctgacagaataatgagac	380		

QY	352	-----gcggccctggatataatgactcggggtgaagctacccctgtcaacgcctcccta	405
Db	381	tatagtaacaaactggtacttcgctcgggcgaagaaggacccctggtaccgcctcccta	440
RESULT	14		
AAAL1622			
ID	AAAL1622	standard; DNA; 2071 BP.	
AC	AAAL1622;		
XX			
DT	08-AUG-2000	(first entry)	
XX			
DE	Humanised HFE7A designed heavy chain DNA #2.		
XX			
KW	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;		
KW	anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;		
KW	dermatological; immunosuppressive; thymometric; antirheumatic; anti-Fas		
KW	neuroprotic; antilinfertility; neuroprotective; antiartherosclerotic;		
KW	hepctrotropic; humanized; apoptosis; systemic lupus erythematosis;		
KW	Hashimoto disease; rheumatoid arthritis; graft versus host disease;		
KW	Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;		
KW	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;		
KW	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;		
KW	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;		
KW	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.		
XX			
OS	Synthetic.		
XX			
PN	EP90663-A2.		
XX			
PD	05-APR-2000.		
XX			
PF	29-SEP-1999; 99EP-0307711.		
XX			
PR	30-SEP-1998; 98JP-0276881.		
PR	30-SEP-1998; 98JP-0276882.		
XX			
PA	(SANY ) SANKYO CO LTD.		
XX			
PI	Serizawa N, Haryuama H, Nakahara K, Tamaki I, Takahashi T;		
XX	WPI; 2000-258930/23.		
DR	P-PSDB; AAW90929.		
PT	New humanized anti-Fas antibody, useful for treating or preventing e.g.		
PT	Inflammatory or autoimmune disease, induces apoptosis selectively in		
XX	cells with abnormal Fas-Fas ligand systems		
PS	Example reference 22; Page 148-150; 263pp; English.		
XX			
CC	This invention describes a novel humanized anti-Fas antibody-like		
CC	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas		
CC	ligand system, by binding to Fas on the cell surface, and prevents		
CC	apoptosis in cells with a normal system, by inhibiting binding between		
CC	Fas and its ligand. The products of the invention have anti-inflammatory		
CC	anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,		
CC	immunomodulatory, dermatologic, immunosuppressive, thymometric,		
CC	antirheumatic, nephrotropic, antilinfertility, neuroprotective,		
CC	antiartherosclerotic, cardiant and hepatropic activity. (I) induce		
CC	apoptosis by binding to cell surface Fas or inhibit it by competitive		
CC	inhibition of ligand binding. (I) are used to treat and/or prevent		
CC	diseases associated with the Fas/Fas ligand system, especially systemic		
CC	lupus erythematosis, Hashimoto disease, rheumatoid arthritis, graft		
CC	versus host disease, Sjorgen's syndrome, pernicious or hypoplastic		
CC	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's		
CC	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,		
CC	multiple sclerosis. Basedow's disease, thrombopenia purpura, insulin		
CC	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,		
CC	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral		
CC	(B, C or D) or alcoholic), and transplant rejection. (I) selectively		
CC	inhibit apoptosis in normal cells but selectively induce it in abnormal		

cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody HFE7A designed heavy chain which is used in the method described in the invention.

Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 62.6%; Score 253.6; DB 21; Length 2071;  
Best Local Similarity 77.6%; Pred. No. 5,9e-60;  
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

```
OY 1 atgggttggaactatcatcttcttctgtaccacagctggtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 21 atggatgtgagctgtatcatctctctgtgtagaacagctggtccactcag 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 61 gtccagctggtgacgtctgggctggaagagctggagctcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 81 gtccaactggtgcagctcgtggctggaagagctgggcttcagtgaaagtgtcc 140
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 121 tgcgaagcttcgcgtacacatcatcgtatctatcagctggtgagcagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 141 tgcgaagcttcgtgtacacctcaccagctcagctgagctggttaaacagccct 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 181 ggcagggcctcgtggtgattggaattataattactgtataacacatacacaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 201 ggcagggcctcgtggtgattggaattactcctctgtatagctatacactacaac 260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 241 cagaagtttaaggcgaagggccacatgactgtagaacaagtcgaagcagcagctatgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 261 caaagttcaaggcgaagggccacatgactgtagaacaagtcgaagcagcagctatgt 320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 301 gaactagcttcttgagatcgtgagatagcgcgtttactgtggaaga----- 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 321 gagctcagcagctcgtgagatcgtgagacagcgcgttctactctgtgcaagaatacggac 380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 352 -----gcgcctgtgtatgtgactactggtggaaggtaccctgttaccgttccctca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 381 tatagtaaacactgttactcgtactgctgtggtggaagggaccctgttaccgttccctca 440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

RESULT 15

AAAI1644 standard; DNA; 2073 BP.

AAAI1644;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Neu 1 DNA.

Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
dermatological; immunosuppressive; thymomatous; antirheumatic; anti-Fas;  
hepatotropic; antifertility; neuroprotective; antiarteriosclerotic;  
neurotrophic; humanized; apoptosis; systemic lupus erythematosus;  
Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
Storjen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY ) SANKYO CO LTD.

PI Serizawa N, Haryama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI: 2000-258930/23.

DR P-PSDB; AAW90933.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems

Claim 33; Page 166-168; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymomatous, antirheumatic, nephrotropic, antifertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Storjen's syndrome, penitons or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence encodes a humanised anti-Fas antibody heavy chain construct designated Neu 1 which is described in the method of the invention.

Sequence 2073 BP; 462 A; 685 C; 559 G; 367 T; 0 other;

Query Match 62.2%; Score 252; DB 21; Length 2073;  
Best Local Similarity 77.4%; Pred. No. 1.6e-59;  
Matches 325; Conservative 0; Mismatches 80; Indels 15; Gaps 1;

```
OY 1 atgggttggaactatcatcttcttctgtaccacagctcagctggtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 23 atggatgtgagctgtatcatctctctgtgtagaacagctggtccactcag 82
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 61 gtccagctggtgacgtctgggctggaagagctggagctcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 83 gtccaactggtgcagctcgtggctggaagagctgggcttcagtgaaagtgtcc 142
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 121 tgcgaagcttcgcgtacacatcatcgtatcgtatacagctggtgagcagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 143 tgcgaagcttcgtgtacacctcaccagctactggaagcagctggttaaacagccct 202
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 181 ggcagggcctcgtggtgattggaattataattactgataaacaacaacacacac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 203 ggcagggcctcgtggtgattggaattactcctctgtatagctatacactacaac 262
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 241 cagaagtttaaggcgaagggccacaatgactgtagaacaagtcgaagcagcagctatgt 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 263 caaagttcaaggcgaagggccacaatgactgtagaacaacacacacacacacacac 322
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
OY 301 gaactagcttcttgagatcgtgagatagcgcgtttactgtggaaga----- 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

Db 323 gagctcagcagcctgagatctgagacacgcggtctattactgtgcaagaataagggac 382  
Oy 352 -----gcggccttggtataggaactactggggtcaaggtacccttgtcacccgtctcctca 405  
Db 383 tatagtacaacactggtactctcgatgtctgggccaaggtacacactgtlcaaccgtctcctca 442

Search completed: August 26, 2002, 16:19:48  
Job time: 4482 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:04:11 ; Search time 60.31 Seconds

(without alignments)  
1649.504 Million cell updates/sec

Title: US-09-249-011-5

Perfect score: 405  
Sequence: 1 atgggttgacgtatcatc.....cccttgaccctcctca 405

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 363533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/prodata/2/lna/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/lna/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/lna/PCUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277.2	68.4	524	5	Sequence 4, Appl1
2	254.4	62.8	424	4	Sequence 62, Appl1
3	253.6	62.6	451	4	Sequence 11, Appl1
4	253.6	62.6	451	5	Sequence 11, Appl1
5	248.2	61.3	433	1	Sequence 11, Appl1
6	248.2	61.3	433	1	Sequence 11, Appl1
7	245	60.5	405	1	Sequence 68, Appl1
8	245	60.5	405	1	Sequence 68, Appl1
9	245	60.5	405	1	Sequence 68, Appl1
10	245	60.5	405	1	Sequence 68, Appl1
11	245	60.5	405	1	Sequence 68, Appl1
12	240.8	59.5	421	3	Sequence 62, Appl1
13	238.6	58.9	433	1	Sequence 18, Appl1
14	238.6	58.9	433	1	Sequence 18, Appl1
15	238.6	58.9	433	1	Sequence 18, Appl1
16	238.6	58.9	433	1	Sequence 18, Appl1
17	238.6	58.9	433	4	Sequence 18, Appl1
18	237.6	58.7	422	1	Sequence 77, Appl1
19	237.6	58.7	422	1	Sequence 77, Appl1
20	237.6	58.7	422	2	Sequence 77, Appl1
21	237.6	58.7	422	2	Sequence 77, Appl1
22	237.6	58.7	422	2	Sequence 77, Appl1
23	237.6	58.7	422	2	Sequence 77, Appl1
24	237.6	58.7	422	2	Sequence 77, Appl1
25	237.6	58.7	422	3	Sequence 77, Appl1
26	236.8	58.5	409	4	Sequence 98, Appl1
27	236	58.3	421	3	Sequence 73, Appl1

28	234.4	57.9	421	3	US-08-836-561-77	Sequence 77, Appl1
29	233.6	57.7	408	5	PCT-US93-11611-3	Sequence 3, Appl1
30	232.8	57.5	429	1	US-08-236-520-6	Sequence 6, Appl1
31	232.8	57.5	429	5	PCT-US95-05262-6	Sequence 26, Appl1
32	232.2	57.3	405	1	US-08-137-117D-26	Sequence 26, Appl1
33	232.2	57.3	405	1	US-08-436-717-26	Sequence 26, Appl1
34	231.4	57.1	461	2	US-07-916-098A-39	Sequence 39, Appl1
35	231.4	57.1	2560	2	US-07-916-098A-44	Sequence 44, Appl1
36	231.4	57.0	433	3	US-08-673-799C-99	Sequence 82, Appl1
37	229.6	56.7	421	3	US-08-836-561-82	Sequence 60, Appl1
38	229.4	56.6	432	2	US-08-673-799C-60	Sequence 60, Appl1
39	229.4	56.6	432	2	US-08-673-799C-60	Sequence 60, Appl1
40	227.4	56.1	461	4	US-09-096-244-3	Sequence 3, Appl1
41	227	56.0	386	4	US-09-199-149-11	Sequence 11, Appl1
42	227	56.0	1572	1	US-08-353-400-23	Sequence 23, Appl1
43	226.2	55.9	433	3	US-08-673-799C-100	Sequence 100, Appl1
44	226.2	55.9	433	3	US-08-673-799C-101	Sequence 101, Appl1
45	226	55.8	414	1	US-07-634-278-84	Sequence 84, Appl1

#### ALIGNMENTS

RESULT 1  
PCT-US91-02942-4  
Sequence 4, Application PC/TUS9102942  
GENERAL INFORMATION:  
APPLICANT: ROTHELEIN, ROBERT  
APPLICANT: ADAIR, JOHN R  
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Ave. NW Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/02942  
FILING DATE: 19910429  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9009549.8  
FILING DATE: 27-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: FOX, SAM L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 1011.0586600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 466-0800  
TELEFAX: (202) 833-8716  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 524 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: Both  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 34..522  
PCT-US91-02942-4

Query Match 68.4%; Score 277.2; DB 5; Length 524;  
Best Local Similarity 81.4%; Pred. No. 3.2e-81;





```

: ATTORNEY/AGENT INFORMATION:
: NAME: Liebescheut, Joe O.
: REGISTRATION NUMBER: 37,505
: REFERENCE/DOCKET NUMBER: 11823-002220
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 451 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 12..431
: US-08-579-378A-11

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Query Match      62.6%; Score 253.6; DB 4; Length 451;
Best Local Similarity 77.6%; Pred. No. 1.5e-73;
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

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QY 1 atgggttggaactgtatcatcttcttctgttaccacagctacaggtgtgactccag 60
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DB 12 ATGGGATGAGCTGTATCATCTCTCTTGTAGCAACAGCTACAGGTGTCACCTCCAG 71
QY 61 gtccagctgtgacgtctgaggtgaggaagcctggaagctcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 72 GTCAGCTGTGACAGTGTGAGCTGAAGTCAAGAACTGGAGACTCAGTGAAGGTATCC 131
QY 121 tgcgaagcttcgagctacacattcattatgatacagtggtgagacagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 TGCAGAGCTTCTGTGATACACATTCATGATGTATGCACTGGTGAGACAGGACACT 191
QY 181 ggaagagggcctcgaagtgtgaggtatgaattactatgataatacaactaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 GGTCAAGAGACTCGATGGATTGGATATTTATCTTACAAATGATGATCAAGTACAT 251
QY 241 cagaagtttaagggcaagccacaatgactgtagacaagctgacagacacagctata 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 252 GAGAAAGTTCAAGGCCGCGATCACAATTTACTTACAGCAGTCACTAACACAGCCTACATG 311
QY 301 gaactagttcttgaagatctgagatacagcgcttatactgtgcaagagcgacct-- 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 312 GAACCTGACAGCTTGCGATCGGAGGACACTGCACTATTACTGTGCAAGGAGAGATAT 371
QY 359 -----gatatagactactggggtcgaaggtaccctgtgcaagcgctctca 405
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DB 372 GGTACTACTGTTGCGTACTTGATGTCTGGGGCCCAAGGTACTGTGTCACAGTCTCTCA 431

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RESULT 4
PCT-US93-11612-11
: Sequence 11, Application PC/TUS9311612
: GENERAL INFORMATION:
: APPLICANT: Co. Man Sung
: TITLE OF INVENTION: Humanized Antibodies Reactive with
: TITLE OF INVENTION: L-Selectin
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/11612
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/983,946
: FILING DATE: 01-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 451 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 12..431
: PCT-US93-11612-11

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Query Match      62.6%; Score 253.6; DB 5; Length 451;
Best Local Similarity 77.6%; Pred. No. 1.5e-73;
Matches 326; Conservative 0; Mismatches 79; Indels 15; Gaps 1;

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QY 1 atgggttggaactgtatcatcttcttctgttaccacagctacaggtgtgactccag 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 12 ATGGGATGAGCTGTATCATCTCTCTTGTAGCAACAGCTACAGGTGTCACCTCCAG 71
QY 61 gtccagctgtgacgtctgaggtgaggaagcctggaagctcagtgaaagtgtcc 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 72 GTCAGCTGTGACAGTGTGAGCTGAAGTCAAGAACTGGAGACTCAGTGAAGGTATCC 131
QY 121 tgcgaagcttcgagctacacattcattatgatacagtggtgagacagctcct 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 132 TGCAGAGCTTCTGTGATACACATTCATGATGTATGCACTGGTGAGACAGGACACT 191
QY 181 ggaagagggcctcgaagtgtgaggtatgaattactatgataatacaactaac 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 GGTCAAGAGACTCGATGGATTGGATATTTATCTTACAAATGATGATCAAGTACAT 251
QY 241 cagaagtttaagggcaagccacaatgactgtagacaagctgacagacacagctata 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 252 GAGAAAGTTCAAGGCCGCGATCACAATTTACTTACAGCAGTCACTAACACAGCCTACATG 311
QY 301 gaactagttcttgaagatctgagatacagcgcttatactgtgcaagagcgacct-- 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 312 GAACCTGACAGCTTGCGATCGGAGGACACTGCACTATTACTGTGCAAGGAGAGATAT 371
QY 359 -----gatatagactactggggtcgaaggtaccctgtgcaagcgctctca 405
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 372 GGTACTACTGTTGCGTACTTGATGTCTGGGGCCCAAGGTACTGTGTCACAGTCTCTCA 431

```

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RESULT 5
US-08-137-117D-111
: Sequence 11, Application US/08137117D
: Patent No. 5795965
: GENERAL INFORMATION:
: APPLICANT: TSUCHIYA, Masayuki
: APPLICANT: SATO, Koh
: APPLICANT: BENDIG, Mary
: APPLICANT: JONES, Steven
: APPLICANT: SALDANHA, Jose
: TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
: INTERLEUKIN-6 RECEPTOR
: NUMBER OF SEQUENCES: 158

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117D
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 16..420
NAME/KEY: mat_peptide
LOCATION: 16..420
US-08-137-117D-111

Query Match 61.3%; Score 248.2; DB 1; Length 433;
Best Local Similarity 75.8%; Pred. No. 8,7e-72;
Matches 307; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 atgggttggaactgtatcatctctcttcgtgtaccacagctacaggtgtgactccag 60
Db 16 atgacacgtgacacttgagaggtcttctgtctgtgctgtagctgacgtccagctcaccag 75
Qy 61 gtccagctggtctgcaagctgaggtggaagaagcctggagctcaagtgaaggtctcc 120
Db 76 gtgcagcttgcagctgagctgaggtggaagaagcctggagctcaagtgaaggttcc 135
Qy 121 tgcagaagctccgagctcacatctacatgctatagctatagctgaggaagcagccct 180
Db 136 tgcagaagcttctgcatctcatttacttacttacttacttacttacttacttactt 195
Qy 181 ggaacagagctcagtgatgtgagttatataatcttacttacttacttacttactt 240
Db 196 ggacaaagccttgatgtgagttatataatgaccccttgcacgtgagttatataat 255
Qy 241 cagaagtttaaggaagcaagcaatgacgtgtagaagaagtcagacagcagcctatag 300
Db 256 cagaagtttaaggaagcaagcaatgacgtgtagaagaagtcagacagcagcctatag 315
Qy 301 gaactgtctcttgaagatctgagataagcgcttacttacttacttacttacttactt 360
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Db 316 gagctgacagctgacatctgacagacacgcctgtgattactgtgcagagcggtaac 375
Qy 361 tatatgactctctgggtcgaaggtacccctgttaccgctctccta 405
Db 376 cgcttgcttactgtgaggaacccctggtcacccgtctccta 420

RESULT 6
US-08-436-717-111
Sequence 111, Application US/08436717
Patent No. 5817790
GENERAL INFORMATION:
APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
FILING DATE: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-32084
FILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/126/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 16..420
NAME/KEY: mat_peptide
LOCATION: 16..420
US-08-436-717-111

Query Match 61.3%; Score 248.2; DB 1; Length 433;
Best Local Similarity 75.8%; Pred. No. 8,7e-72;
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	Matches, 307;	Conservative	0;	Mismatches	98;	Indels	0;	Gaps	0;
OY	1	atgggttggaactgatactatcattcttcttttgttaccacaagctcaagggtgtgacatccaa	60						
Dd	16	ATGGAGCTGACCTGGAGGGGTCTTCTTTGCTGGCTGTAGCTCCAGTGCTCACCAG	75						
OY	61	gtccagctgtgtgcagtctctgtgggtctgaagtgaaagacctgtggagtcagtgaaagtgatcc	120						
Dd	76	GTCAGCTGTGNTGCACACTGTGAGACTGAGGTGAAGAAGACCTGGGGGCTCATGTAAAGGTTGCC	135						
OY	121	tgcagaagtttcgcggttacacattcacctgatattgctatacagtggtgtgtagaagagctct	180						
Dd	136	TGCAAGSGTTCTCGAAGTCACTCATCTGTTATTATACATAACATCTGGGTGCGCACGCCCCC	195						
OY	181	ggacagggcccctcgagatgtgagatltgaatlaataattaactgatatataaacacacacaac	240						
Dd	196	GGACAAGAGCTTGAGTGGATGGGATATATTATGACCCCTTTCANATNGTGTACTAGCTATATAT	255						
OY	241	cagaagtttaaggagccaagccacaatgactgtagaacaagtgcagagacagacgcatatag	300						
Dd	256	CAGAAGTTTCAAGGGCAGAGTCAACCATTTACCGTAGACATCCGCGACAGACACACCTTACATG	315						
OY	301	gaacttagtctcttgagatcttgagatatacggccgttttatctgtgtgcaagagcggccatg	360						
Dd	316	GAGCTGACACTGTCTAGATCTGTGAAGACACAGCGCTGTGTATTACTGTGTGCGAGAGGGGGTAAC	375						
OY	361	tatatgactactgtgggtcaagytacaccttgcacgcttcctca	405						
Dd	376	CGCTTGTCTACTGTGGGCGCAGGAGACCTGTGTCACCGTCTCTCA	420						
<b>RESULT 7</b>									
	US-07-634-278-68								
	Sequence 68, Application US/07634278								
	Patent No. 5530101								
	GENERAL INFORMATION:								
	APPLICANT: QUEEN, Cary L.								
	APPLICANT: CO, Man Sung								
	APPLICANT: SCHNEIDER, William P.								
	APPLICANT: LANDOLET, Nicholas F.								
	APPLICANT: COELINGH, Kathleen L.								
	APPLICANT: SELICK, Harold E.								
	TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS								
	NUMBER OF SEQUENCES: 113								
	CORRESPONDENCE ADDRESS:								
	ADDRESSEE: Townsend and Townsend Khourie and Crew								
	STREET: 379 Lytlton Avenue								
	CITY: Palo Alto								
	STATE: California								
	COUNTRY: US								
	ZIP: 94301								
	COMPUTER READABLE FORM:								
	MEDIUM TYPE: Floppy disk								
	COMPUTER: IBM PC compatible								
	OPERATING SYSTEM: PC-DOS/MS-DOS								
	SOFTWARE: Patentin Release #1.0, Version #1.25								
	CURRENT APPLICATION DATA:								
	APPLICATION NUMBER: US/07/634,278								
	FILING DATE: 19-DEC-1990								
	CLASSIFICATION: 424								
	PRIOR APPLICATION DATA:								
	APPLICATION NUMBER: US 07/590,274								
	FILING DATE: 28-SEP-1990								
	PRIOR APPLICATION DATA:								
	APPLICATION NUMBER: US 07/310,252								
	FILING DATE: 13-FEB-1989								
	PRIOR APPLICATION DATA:								
	APPLICATION NUMBER: US 07/290,975								
	FILING DATE: 28-DEC-1988								
	ATTORNEY/AGENT INFORMATION:								
	NAME: Smith, William M								
	REGISTRATION NUMBER: 30,223								
	REFERENCE/DOCKET NUMBER: 11823-002600								

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..405
US-07-634-278-68

Query Match      60.5%; Score 245; DB 1; Length 405;
Best Local Similarity 75.3%; Pred. No. 9,4e-71;
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Oy      1 atgggttggaactgcatcattcttcttcgtgtaccacagctcacagtgtgcactccag 60
Db      1 ATGGGATGTGAGCTGGATCTTCTTCCTCCCTCGTAGAAGACTGCAGGGCTCACCTTGAG 60

Oy      61 gtccagctcggtgcagttctcgggctgaaagaaacctggagctcaagtatgcc 120
Db      61 GTCCAGCTTCAGCACTCAGGACCTGAGCTGGTGAACAACCTGGGGCCCTCAGTGAAAGATTACC 120

Oy      121 tgcagaagcttcgggtaccatactcgtatgatgtatatacagtggtggtagaacagctct 180
Db      121 TGCAGAAGCTTCGGGTATACACTCTCATCTCAACATGCACTGGGTGAGCAGAGACCTAT 180

Oy      181 ggcacaggccttcagatgtgattggagttattaatatctactatgataataacaactaac 240
Db      181 GGAAGAGACCTTGATGTGATTGATATATTATTTATCCCTTAATGCTGGTACTGGCTAAC 240

Oy      241 cagaaggttaagggaagggccaatgactgtaagcaagtgcagagcaagccatctatg 300
Db      241 CAGAAGTTCAMAGGCAAGGCCACATTGACTGTAGCAAAATCTCCAAGCACAGCTTACATG 300

Oy      301 gaacttagtctctcgtagatctcgtagatalcagcgcttattactgtgcgaagacggcttgg 360
Db      301 GACGTCGCCAGCCTGACATCTGAGACTGAGAGACTGTCGACGTCATTACTGTGCAAGAGGGCCCC 360

Oy      361 tatatgactactagggtgtcaaggtacacctgtgcacctctccta 405
Db      361 GCTATGAGACTACTGGGGTCAAGGAACCTCAGTACACCGTCTCTCTCA 405

RESULT      8
US-08-477-728-68
; Sequence 68, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728

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FILED DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
US-08-477-128-68

Query Match 60.5% Score 245; DB 1: Length 405;  
Best Local Similarity 75.3%; Pred. No. 9.4e-71;  
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctacaggtgtgactccag 60  
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QY 61 gtccagcttgcagctctgagctgaggttgagaagcctggagctcagtgaaagtctc 120  
DB 61 GTCAGCTTCAGCAGTACAGGAGCTGAGCTGGAACCTGGGGCTCAGTAAATATCC 120  
QY 121 tgcgaagcttcgagctacacatctacatgattatgatacagtggtgagcagctcct 180  
DB 121 TGCAGGCTTGTGATACACATTCACCTGACACATGCACTGGGTGAAGCAGCCAT 180  
QY 181 ggacagggcctcgagctgagattgagattataataattactatgataatacaactacaac 240  
DB 181 GGAAGAGGCTTGTGATGATATATATTCCTTACATGATGATGATGCTGACAAAC 240  
QY 241 cagaagtttaagggcaagggccacaatgactgtacacaagctgagaagcagcgtctatg 300  
DB 241 CAGAAGTTCAAGACCAAGGCCACATTCAGCTGTAGACAATTCCTCAGACAGCCTTACATG 300  
QY 301 gaacttgcttcctgagatcctgagatacggcgttactactgtgcaagcgcgctcctg 360  
DB 301 GACTCCGCGAGCCCTGACATCTGAGGACTCTGCACTCTATTCTGTGCAAGGCGGCCCC 360  
QY 361 tatatggaactactggtggttcaaggtacacctgtgacacgctctcctca 405  
DB 361 GCTATGAGCTACTGGGGTCAAGGAACCTCACTCAACCGTCTCTCA 405

RESULT 9  
US-08-474-040-68  
Sequence 68, Application US/08474040  
Patient No. 5693761  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.

APPLICANT: CO., Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINCH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,040  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
US-08-474-040-68

Query Match 60.5% Score 245; DB 1: Length 405;  
Best Local Similarity 75.3%; Pred. No. 9.4e-71;  
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atgggttggaactgtatcatcttcttctgttaccacagctacaggtgtgactccag 60  
DB 1 ATGGGATGAGAGCTGATCTTCTCTCTCTCTGACAGAACTGACGGCTCACCTGAG 60  
QY 61 gtccagcttgcagctctgagctgaggttgagaagcctggagctcagtgaaagtctc 120  
DB 61 GTCAGCTTCAGCAGTACAGGAGCTGAGCTGGAACCTGGGGCTCAGTAAATATCC 120  
QY 121 tgcgaagcttcgagctacacatctacatgattatgatacagtggtgagcagctcct 180  
DB 121 TGCAGGCTTGTGATACACATTCACCTGACACATGCACTGGGTGAAGCAGCCAT 180  
QY 181 ggacagggcctcgagctgagattgagattataataattactatgataatacaactacaac 240  
DB 181 GGAAGAGGCTTGTGATGATATATATTCCTTACATGATGATGCTGACAAAC 240

OY 241 cagaagtttaagggaagccacaatgactgttagaagaagtcgacgagcacagcctataty 300  
|||||  
Db 241 CAGAAGTTCAAGACCAAGCCACATGTGACTGTAGACATTCCTCCAGACAGACCTACATG 300  
OY 301 gaacttgcttcttgagctcgtgagatagcgccgtttattctgtgcaagagcgccctg 360  
|||||  
Db 301 GAGCTCCGACCCGTGACATCTGAGGACTCTGACGTATTACTGTGCAAGAGGGCGCC 360  
OY 361 tataatgactctggggtcaaggtacccctgtcacgcgtctctca 405  
|||||  
Db 361 GCTATGACTACTGGGCTCAAGGAACCTCAGTCAACCGTCTCTCA 405

RESULT 10  
US-08-487-200-68  
Sequence 68, Application US/08487200  
Patent No. 5693762

GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,200  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002610  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
US-08-487-200-68

Query Match 60.5%; Score 245; DB 1; Length 405;  
Best Local Similarity 75.3%; Pred. No. 9.4e-71;  
Matches 305; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

OY 1 atgggttggaactatcatcttcttctgtgtaccacagctaaagtgtgactccag 60  
|||||  
Db 1 ATGGATGAGAGCTGATCTTCTCTCCCTGTCAGGAACCTGACGGCTCCACTCTGAG 60  
OY 61 gtccagctggtgcaactctggggctgagtgaaagacgttggaagctgaagtgtgccc 120  
|||||  
Db 61 GTCCAGCTTCACAGCTCAGGACCTGAGCTGTGAAACCTGGGGCTCTGAGTAATATCC 120  
OY 121 tgcagaagctccggtacacattcactgattatgtatatacagtggtgtagaagcgtcc 180  
|||||  
Db 121 TGCAAGGCTTTCGATGATACATCTGACTGATCAACATGCACTGGGTGAGAGGACAT 180  
OY 181 ggcagagcctcagtgagtgagtgatlaataattactatgataatacaactacaac 240  
|||||  
Db 181 GGAAGAGCCTTGAGTGATGATGATATTTATCTTCAATGATGATGATGATGATGATGAT 240  
OY 241 cagaagtttaagggaagccacaatgactgtagaagagtgacgagcacagcctatg 300  
|||||  
Db 241 CAGAAGTTCAAGACCAAGCCACATTTGACTGTAGCAATTCCTCCAGACAGCCTACATG 300  
OY 301 gaacttgcttcttgagatctgagatagcgccgtttattctgtgcaagagcgccctg 360  
|||||  
Db 301 GAGCTCCGACCCGTGACATCTGAGGACTCTGACGTATTACTGTGCAAGAGGGCGCC 360  
OY 361 tataatgactctggggtcaaggtacccctgtcacgcgtctctca 405  
|||||  
Db 361 GCTATGACTACTGGGCTCAAGGAACCTCAGTCAACCGTCTCTCA 405

RESULT 11  
US-08-484-537-68  
Sequence 68, Application US/08484537  
Patent No. 6180370

GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: COELINGH, Kathleen L.  
APPLICANT: SELICK, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,537  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..405  
US-08-484-537-68

Query Match	60.5%	Pred. 245;	DB 4;	Length 405;
Best Local Similarly	75.3%	Pred. No. 9.4e-71;		
Matches 305; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	1	atgggttggaaactatcatctcttcttcgtgtctccaaagctaaagtttgcactccag	60
Db	1	ATGGGATGGACCTGGATCTTCTCTCTCTCTGTCAGGAACGTGAGGCGTCCACTTCGAG	60
QY	61	gtccaaagctctgcagctctgggctcgaagtgaaagaagcctggagctcaatgaaagtctcc	120
Db	61	GTCGAGCTTCAGACAGTCAAGACCTCGAGCTGGTGAACCTGGGGCTCAGTCMAATATCC	120
QY	121	ttgcaaaagcttccggctacacatactcatgatathgctatacagttgggttgaaagagctcct	180
Db	121	TGCAAGGCTTCTGGATACACATTCCTACATGACTACAACATGCACTGGTGAAGCAAGCCAT	180
QY	181	ggacaagggcccctcggtgatctggggttatataatttaccatgatataataacaataaac	240
Db	181	GGAAAGACCCCTTGATGGATGGATTGGATATATATATCTTTACAATGGTGGTATCGGCTTAAC	240
QY	241	cagaagtttaaggccaagggccacacatgacttgacaagatcgaaagcaacagctcatatg	300
Db	241	CAGAAGTTCAAGAGACCAAGGCCACATTGACTCTAACAATTCCTCCAGCAGCCTTAATG	300
QY	301	gaacttagttcttgagatctcgaagataagggccgtttatattactgtgcaagagcggcttg	360
Db	301	GAGCTGCCGACCTGACATCTGAGAGACTCTGCACTATATTACTGTGCAAGAGGGCGCCC	360
QY	361	tatatgactactcgggttcaaggttaacctgtgtacacgctctccta	405
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RESULT 12  
US-08-836-561-62  
Sequence 62, Application US/08836561  
Patent No. 6018032  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
APPLICANT: FURUYA, AKIKO  
APPLICANT: NAKAMURA, Kazuyasu  
APPLICANT: IIDA, Akihito  
APPLICANT: ANAZAWA, Hideharu  
APPLICANT: HANAI, No. 6018032uo  
APPLICANT: TAKATSU, Takashi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
TITLE OF INVENTION: Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Pennile & Edmonds LLP  
STREET: 1155 Avenue of the Americas

```

1 CITY: New York
2 STATE: NY
3 COUNTRY: USA
4 ZIP: 10036
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Diskette
8 COMPUTER: IBM Compatible
9 OPERATING SYSTEM: DOS
10 SOFTWARE: FastSEO Version 2.0
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/836,561
13 FILING DATE: 09-MAY-1997
14 CLASSIFICATION: 424
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: JP 23284/95
17 FILING DATE: 11-SEP-1995
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Lawrence, III, Stanton T
20 REGISTRATION NUMBER: 25,736
21 REFERENCE/DOCKET NUMBER: 7005-115-999
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 212-790-9090
24 TELEFAX: 212-869-9741
25
26 TELEX: 66141 PENNIE
27 INFORMATION FOR SEQ ID NO: 62:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 421 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 MOLECULE TYPE: Other
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35 US-08-836-561-62

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Query Match	59.58;	DB 3;	Length 421;
Best Local Similarity	75.78;	Pred. No. 2.3e-69;	
Matches 318; Conservative	0;	Mismatches 87;	Indels 15; Gaps 1;

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Db	61	GTCACAGCTGG	TGCAGTCTGGAGACTTGAGGTAA	GAAGCCTGGGGCTTTAGTGAAGTTCC	120					
Oy	121	tgcaaagcttc	cggtctacaca	ttcaactg	atatycta	acagtygt	gtgaa	caggtc	ctt	180
Db	121	TGCAAGGCTTC	TGGATACACATTCATAGATTATTTATTC	ACTGGTGCCACAGGCCCTT	180					
Oy	181	ggacagggccc	caggtgatgt	ggatgata	taataat	tttttttt	tttttttt	tttttt	taac	240
Db	181	GGTCAAGGCCCTT	TGATGGATGGGATATATTTATATCTT	TACATGATGGGACTTAAGTACAAT	240					
Oy	241	cagaagttta	aggccaagcc	acacatgact	gtagaca	agtcga	agagacac	agccata	tg	300
Db	241	GAGAGGTTCAA	AGGCGAGAGTACACATCACTG	CACACACGTCCACAGCACAGCCTACATG	300					
Oy	301	gaacttagt	tctctt	ggagatc	tggagata	cggcgctt	tatact	ctgtc	caag	352
Db	301	GAGCTCAAT	TGCTGTGAGATCTGAGAGACACG	CGGTGTATTA	CTGTGCGAGAGAAGGAAATT	350				
Oy	353	-----cg	gcctgtata	tatgag	tactggg	tataag	taccc	ttgcac	gcgtct	405
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RESULT 13  
US-07-634-278-18  
; Sequence 18, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.

```

APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: APOLDOFT, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 6..410
OTHER INFORMATION: /product= "Humanized anti-Tac heavy
OTHER INFORMATION: chain variable region," Seq ID. 19"
US-07-634-278-18

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Query Match	58.9%	Score 238.6	DB 1	Length 433
Best Local Similarity	74.3%	Pred. No. 1,2e+68		
Matches 301	Conservative 0	Mismatches 104	Indels 0	Gaps 0
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Db 6	ATGGGATGGACGTGGATCTTCTCTCCCTCGTAGGATCCGGCGGGCTGACACTCTG	65		
QY 61	gtccagctcgtgtgcactcctcggggtctgaagtgaagaacctctggagctcagtgaaagtgtcc	120		
Db 66	GTCAGCTTGTCACACTCTGGGGCTGAAGTCAAGAAACCGCTCTCAGACTGAAGGTCCTC	125		
QY 121	tgcgaagcttcgcggtacacatacctacgtatgaatgtatacagttgggtggaagaagctcct	180		
Db 126	TGCAAGCGTTCTGGGTACACCTTTCACCTTACCTACAGAGATGCACTGGGTAAAGCAGGCCCTT	185		
QY 181	ggacaggagcctcgaattggaattggaatttaataattcaatgatataataacaactacaac	240		

Db	186	GCAGCAGGATCTGCAATGGATTTGATATATTATATCCGTGACGTGGATTTACGATTAACAAT	245
Qy	241	cagaagtttaagygccaagccacaatgactgttagacaagtgcagcagcaagctatatg	3000
Db	246	CAGTAAGTTCAAGGCAAGGGCAACATTATCTGCAGACCAATTCACCAATACAGCCTACATG	3050
Qy	301	gaacttgctcttgaagatctgagaatagagcgctttattacgttgaagaagcgccttg	3600
Db	306	GAACTGAGCAACCTCGAATCTGAGAGAACCCCACTATTACTGTGCAAGAGGGGGGGG	3650
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14 RESULT 14
15 US-08-477-728-18
16 ; Sequence 18, Application US/08477728
17 ; Patent NO. 5585089
18 ;
19 ; GENERAL INFORMATION:
20 ;
21 ; APPLICANT: QUEEN, Cary L.
22 ; APPLICANT: SCHNEIDER, William P.
23 ; APPLICANT: SELICK, Harold E.
24 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
25 ; NUMBER OF SEQUENCES: 113
26 ;
27 ; CORRESPONDENCE ADDRESS:
28 ; ADDRESSEE: Townsend and Townsend and Crew LLP
29 ; STREET: Two Embarcadero Center, 8th Floor
30 ; CITY: Palo Alto
31 ; STATE: California
32 ; COUNTRY: US
33 ; ZIP: 94111
34 ;
35 ; COMPUTER READABLE FORM:
36 ; MEDIUM TYPE: Floppy disk
37 ; COMPUTER: IBM PC compatible
38 ; OPERATING SYSTEM: PC-DOS/MS-DOS
39 ; SOFTWARE: Patentin Release #1.0, Version #1.25
40 ; CURRENT APPLICATION DATA:
41 ; APPLICATION NUMBER: US/08/477,728
42 ; FILING DATE: 07-JUN-1995
43 ; CLASSIFICATION: 424
44 ;
45 ; PRIOR APPLICATION DATA:
46 ; APPLICATION NUMBER: US 07/634,278
47 ; FILING DATE: 19-DEC-1990
48 ;
49 ; PRIOR APPLICATION DATA:
50 ; APPLICATION NUMBER: US 07/590,274
51 ; FILING DATE: 28-SEP-1990
52 ;
53 ; PRIOR APPLICATION DATA:
54 ; APPLICATION NUMBER: US 07/310,252
55 ; FILING DATE: 13-FEB-1989
56 ;
57 ; PRIOR APPLICATION DATA:
58 ; APPLICATION NUMBER: US 07/290,975
59 ; FILING DATE: 28-DEC-1988
60 ; ATTORNEY/AGENT INFORMATION:
61 ; NAME: Smith, William M
62 ;
63 ; REGISTRATION NUMBER: 30,223
64 ; REFERENCE/DOCKET NUMBER: 11823-002600
65 ; TELECOMMUNICATION INFORMATION:
66 ; TELEPHONE: (415) 326-2400
67 ; TELEFAX: (415) 326-2422
68 ; INFORMATION FOR SEQ. ID NO: 18:
69 ; SEQUENCE CHARACTERISTICS:
70 ; LENGTH: 433 base pairs
71 ; TYPE: nucleic acid
72 ; STRANDEDNESS: single
73 ; TOPOLOGY: linear
74 ; MOLECULE TYPE: DNA
75 ; HYPOTHEICAL: NO
76 ; FEATURE:
77 ;
78 ; NAME/KEY: CDS
79 ; LOCATION: 6..410
80 ;
81 ; OTHER INFORMATION: /product= "Humanized anti-Tac heavy
82 ; chain variable region, Seq ID. 19"

```

US-08-477-728-18

Query Match                      58.9%: Score 238.6; DB 1; Length 433;  
Best Local Similarity 74.3%: Pred. No. 1.2e-68;  
Matches 301: Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 1 atgggttggaactgatacattcttcttctgttaccacagctaaagtgtgactccag 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 ATGGGATGAGAGCTGGATCTTCTCTCTCTCTCTGACAGTACCGGCGGTCTCAG 65
QY 61 gtccagcttggtgagctggtgagctgaaagcctggagctcagtaagtgctc 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 GTCCAGCTTGCGAGCTGGGGCTGAAGTCAAGAACTGGCTGAGCGTAAGGTCTCC 125
QY 121 tgcgaagcttcgagctacacattcagatgatactgagtggtgagacagctctc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 TGCAGAGCTTCTGGCTACACTTACTAGCTACAGAGTACCTGGTAAAGCAGCCCT 185
QY 181 ggacagggcctcgagtgagtgagtgatataataattactatgataatacaaac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 GGACAGGCTCTGGAATGATGATATATATATATATATATATATATATATATAT 245
QY 241 cagaagcttgaagcgaagcgaacaaatgactgtgaaagctgagcagcagcctatg 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 CAGAAAGTTCAAGGCAAGGCAACAAATTACTGACAGCATTCACCAATATACATG 305
QY 301 gaacttgcttctgagatctgagagatagcgagcttattactgtgcaagagcgcttg 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 GAAGTGAAGCAGCCGTGAATCTGAGAGACACCGCACTTATCTGTGCAAGAGGGGG 365
QY 361 tatatgactactgggtgcaagtgacccctgtgacccgtctctca 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GTCTTTGACTACTGGGGCCAGGAACCTGGTGTACAGTCTCTCA 410
```

RESULT 15

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US-08-474-040-18
; Sequence 18, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Men Sung L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
```

```
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/290,975
;; FILING DATE: 28-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 11823-002600
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 433 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; HYPOTHEICAL: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 6..410
;; OTHER INFORMATION:
;; OTHER INFORMATION: /product="Humanized anti-Tac heavy
;; chain variable region, Seq ID. 19"
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Query Match                      58.9%: Score 238.6; DB 1; Length 433;  
Best Local Similarity 74.3%: Pred. No. 1.2e-68;  
Matches 301: Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 1 atgggttggaactgatacattcttcttctgttaccacagctaaagtgtgactccag 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 ATGGGATGAGAGCTGGATCTTCTCTCTCTCTGACAGTACCGGCGGTCTCAG 65
QY 61 gtccagcttggtgagctggtgagctgaaagcctggagctcagtaagtgctc 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 GTCCAGCTTGCGAGCTGGGGCTGAAGTCAAGAACTGGCTGAGCGTAAGGTCTCC 125
QY 121 tgcgaagcttcgagctacacattcagatgatactgatacagtggtgagacagctctc 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 TGCAGAGCTTCTGGCTACACTTACTAGCTACAGAGTACCTGGTAAAGCAGCCCT 185
QY 181 ggacagggcctcgagtgagtgagtgatataataattactatgataatacaaac 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 GGACAGGCTCTGGAATGATGATATATATATATATATATATATATATATATAT 245
QY 241 cagaagcttgaagcgaagcgaacaaatgactgtgaaagctgagcagcagcctatg 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 CAGAAAGTTCAAGGCAAGGCAACAAATTACTGACAGCATTCACCAATATACATG 305
QY 301 gaacttgcttctgagatctgagagatagcgagcttattactgtgcaagagcgcttg 360
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 GAAGTGAAGCAGCCGTGAATCTGAGAGACACCGCACTTATCTGTGCAAGAGGGGG 365
QY 361 tatatgactactgggtgcaagtgacccctgtgacccgtctctca 405
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GTCTTTGACTACTGGGGCCAGGAACCTGGTGTACAGTCTCTCA 410
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Search completed: August 26, 2002, 16:14:58  
Job time: 4247 sec



Mon Aug 26 17:25:46 2002

us-09-249-011-5.rni

Page 11







C>Date: 02-Apr-1982 #sequence.revision 02-Apr-1982 #text\_change 22-Jun-1999  
C:Accession: A90809; B90809; A22769; A02034; A02036  
R:Borthwell, A.L.M.; Paskind, M.; Retn, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.  
Cell 24, 625-637, 1981  
A>Title: Heavy chain variable region contribution to the NP(b) family of antibodies: som  
A:Reference number: A90809; MOID:81234548  
A:Accession: A90809  
A:Molecule type: DNA  
A:Residues: 1-139 <BI8>  
A:Cross-references: GB:J00529; NID:g195114; PIDN:AAA38170.1; PID:g195115  
A:Accession: B90809  
A:Molecule type: DNA  
A:Residues: 1-117 <I862>  
A>Note: The BI-8 mu chain mRNA was cloned from a hybridoma making antibodies to the hapt  
A>Note: the 186-2 germ-line gene was cloned from a library of C57BL/6 DNA  
RIDldrop, R.; Brugemann, M.; Radbruch, A.; Rajewsky, K.; Beyreuther, K.  
EMBO J. 1, 635-640, 1982  
A>Title: Immunoglobulin V region variants in hybridoma cells. II. Recombination between  
A:Reference number: A90971; MOID:84236026  
A:Accession: A22769  
A:Molecule type: protein  
A:Residues: 20-139 <DI1>  
A>Note: The V region of the BI-8 delta chain, derived as a spontaneous class switch vari  
of the mu chain  
C:Genetics:  
A:introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
F:1-19/DNA: signal sequence #status predicted <SIG>  
F:20-139/Product: Ig kappa chain V region (BI-8) #status experimental <MAT>  
F:34-117/DNA: immunoglobulin homology <IMM>  
F:118-124/Region: D segment  
F:125-139/Region: J segment (JH2)

Query Match 69.6%; Score 501; DB 1; Length 139;  
Best Local Similarity 68.3%; Pred. No. 1e-36;  
Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

OY 1 MGWNCIFLVTTATGVSQVQLVQSGAEVKKPGSSSVKSCASGYFTFDYAIGWVRAP 60  
| | | | | : | | | | | : | | : | | | | | | : | | :  
DB 1 MGWSCIMFLAAATAATGVSHSQVLQQPGAELVKPGASVKLSCASGYFTFSYMHWIKORP 60  
| | | | | : | | | | | : | | : | | | | | | : | | :  
  
OY 61 GGGLLEIVGINITYDMNTYNOKRKATMTVDKSTAFYMEILSRSEDTAYTYCAR-- 117  
| | | | | : | | | | | : | | : | | | | | | : | | :  
DB 61 GGGLLEIVGRIDPNSSGGTFRKRSKATLTVDKPSPSTAYMLSLTSBDSAVYYCARDYD 120  
| | | | | : | | | | | : | | : | | | | | | : | | :  
  
OY 118 -AAWMDYGCGTLTVSSS 135  
| | | | | : | | | | | : | | : | | | | | | : | | :  
DB 121 YGSFYDYMGCGITLVSS 139  
| | | | | : | | | | | : | | : | | | | | | : | | :

RESULT 7  
A27609  
Ig heavy chain precursor V region (129) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Dec-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: A27609  
R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.  
J. Immunol. 140, 1676-1684, 1988  
A>Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switc  
A:Reference number: A27609; MOID:88154467  
A:Accession: A27609  
A:Molecule type: DNA  
A:Residues: 1-139 <KIE>  
A:Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992  
C:Genetics:  
A:introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterodimer; immunoglobulin  
F:1-19/DNA: signal sequence #status predicted <SIG>  
F:20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>  
F:34-117/DNA: immunoglobulin homology <IMM>

Query Match 96.4%; Score 500; DB 2; Length 139;  
Best Local Similarity 68.3%; Pred. No. 1.2e-36;  
Matches 95; Conservative 19; Mismatches 21; Indels 4; Gaps 1;

Oy 1 MGMCNCFEVLVTATGVHSQVOLVQSQAEEVKPKGSSVSCASGCTPTDYAIOWVRQAP 60  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 1 MGMSWIFLFLLSGTAGVLSVEQLQSQGPFLYKPGVASVKMCKASCAGCTPTDYVMHWKQSN 60

Oy 61 GGGLIEWIGVINIYNNTNYNOKFKRKAATMYDKNSTSTAYMELSSLRSDTDVAVYCARAM 120  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 61 GKSLIEWIGVINPYNDYTSTYNOKFKRKAATLVDRKSSSTA YMOILSITSEDSAVYYCARYSY 120

Oy 121 Y----MDYMGCGTTLTVSS 135  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 121 YSYAMDMYMGCGTSTVTVSS 139

RESULT 8  
JL0076

Ig heavy chain precursor V region (anti-phenylloxazalone, 18C10) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 23-Jul-1999  
C:Accession: J10076  
R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.  
Mol. Immunol. 25, 859-865, 1988  
A>Title: Combinatorial association of V genes: one VH gene codes for three non-cross-  
A:Reference number: J10076; MUID:89096973  
A:Accession: J10076  
A:Molecule type: mRNA  
A:Residues: 1141 <KKA>  
A:Cross-references: GB:M2788; NID:g195851; PID:AAA38441.1; PID:g195852  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domn: signal sequence #status predicted <SIG>  
F:20-14/Product: Ig heavy chain #status predicted <MAT>  
F:34-117/Domn: immunoglobulin homology <IMM>  
F:50-54/Region: complementarity-determining 1  
F:69-85/Region: complementarity-determining 2  
F:123-135/Region: J2 segment  
F:136-141/Region: C

Query Match 69.2%; Score 498; DB 2; Length 141;  
Best Local Similarity 69.6%; Pred. No. 1.9e-36;  
Matches 94; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

Oy 1 MGMCNCFEVLVTATGVHSQVOLVQSQAEEVKPKGSSVSCASGCTPTDYAIOWVRQAP 60  
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 1 MGMSWIFLFLLSGTAGVLSVEQLQSQGPFLYKPGVASVKMCKASCAGCTPTDYVMHWKQRP 60

Oy 61 GGGLIEWIGVINIYNNTNYNOKFKRKAATMYDKNSTSTAYMELSSLRSDTDVAVYCARAM 120  
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db 61 GKSLIEWIGVINPYNDYTSTYNOKFKRKAATLVDRKSSSTA YMOILSITSEDSAVYYCAREGP 120

Oy 121 YMDYMGCGTTLTVSS 135  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 121 AGDTYMGCGTTLTVSS 135

RESULT 9  
A32483

Ig heavy chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Aug-1996  
C:Accession: A32483  
R:Larick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck  
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989  
A>Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells  
A:Reference number: A32483; MUID:85273586  
A:Status: preliminary



Cell 24, 625-637, 1981  
A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some  
A:Reference number: A90809; MUID:81234548  
A:Accession: A02038  
A:Molecule type: mRNA  
A:Residues: 1-137 <BON>  
A:Cross-references: GB:00539; NID:g195118; PIND:AAA38172.1; PID:g195119  
A:Note: the gamma-2a chain mRNA was cloned from a hybridoma making antibodies to the hap  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-137/Product: Ig heavy chain V region (SA3) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:118-122/Region: D segment  
F:123-137/Region: J segment (JH2)





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:59:41 ; Search time 15.59 Seconds

(without alignments)  
335,288 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720  
Sequence: 1 MGNMCIFFLVTTATGVHSQ.....ARAAMWDMGQGLTVTVSS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513.5	71.3	136	1	HV15_MOUSE P01759 mus musculu
2	501	69.6	139	1	HV07_MOUSE P01751 mus musculu
3	488	67.8	137	1	HV11_MOUSE P01755 mus musculu
4	487.5	67.7	138	1	HV48_MOUSE P03980 mus musculu
5	483.5	67.2	140	1	HV02_MOUSE P01746 mus musculu
6	470	65.3	117	1	HV06_MOUSE P01750 mus musculu
7	463	64.3	117	1	HV05_MOUSE P01749 mus musculu
8	447	62.1	117	1	HV04_MOUSE P01748 mus musculu
9	444	61.7	117	1	HV1B_HUMAN P01743 homo sapien
10	444	61.7	147	1	HV1C_HUMAN P01744 homo sapien
11	439	61.0	117	1	HV09_MOUSE P01753 mus musculu
12	439	61.0	117	1	HV1G_HUMAN P23083 homo sapien
13	435	60.4	117	1	HV4G_MOUSE P06328 mus musculu
14	429	59.6	117	1	HV10_MOUSE P01754 mus musculu
15	427.5	59.4	117	1	HV13_MOUSE P01757 mus musculu
16	427.5	59.4	120	1	HV03_MOUSE P01747 mus musculu
17	426.5	59.2	117	1	HV12_MOUSE P01756 mus musculu
18	426	59.2	117	1	HV14_MOUSE P01758 mus musculu
19	411	57.1	117	1	HV52_MOUSE P06327 mus musculu
20	408	56.7	118	1	HV51_MOUSE P06330 mus musculu
21	405	56.2	120	1	HV50_MOUSE P06329 mus musculu
22	379.5	52.7	121	1	HV01_MOUSE P01745 mus musculu
23	376.5	52.3	117	1	HV1A_HUMAN P01742 homo sapien
24	374	51.9	114	1	HV00_MOUSE P01741 mus musculu
25	362.5	50.3	125	1	HV1E_HUMAN P06326 homo sapien
26	353	49.0	124	1	HV1D_HUMAN P01760 homo sapien
27	350.5	48.7	121	1	HV3J_HUMAN P01771 homo sapien
28	340.5	47.3	119	1	HV3I_HUMAN P01770 homo sapien
29	339	47.1	122	1	HV3G_HUMAN P01768 homo sapien
30	338	46.9	122	1	HV3H_HUMAN P01769 homo sapien
31	338	46.5	136	1	HV16_MOUSE P01805 mus musculu
32	334.5	46.5	142	1	HV01_RAT P01805 mus musculu
33	334	46.4	124	1	HV1E_HUMAN P01761 homo sapien

34	327.5	45.5	115	1	HV3D_HUMAN P01765 homo sapien
35	324	45.0	114	1	HV01_CANFA P01784 canis fam1
36	324	45.0	119	1	HV37_MOUSE P01807 mus musculu
37	321	44.6	120	1	HV1H_HUMAN P80421 homo sapien
38	319	44.3	119	1	HV38_MOUSE P01808 mus musculu
39	318.5	44.2	119	1	HV3L_HUMAN P01773 homo sapien
40	315	43.8	116	1	HV3F_HUMAN P01781 homo sapien
41	314.5	43.7	117	1	HV42_MOUSE P01812 mus musculu
42	314	43.6	119	1	HV40_MOUSE P01810 mus musculu
43	314	43.6	126	1	HV3K_HUMAN P01772 homo sapien
44	312.5	43.4	144	1	HV43_MOUSE P01819 mus musculu
45	311	43.2	114	1	HV3B_HUMAN P01763 homo sapien

## ALIGNMENTS

```

RESULT 1
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1g heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -----
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CC -----
DR EMBL: J00494; AAA38130.1; -.
DR PIR: A02042; HVMSBL.
DR HSSP: P01772; 2F84.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT NON_TER 136 136
SO SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

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Query Match 71.3%; Score 513.5; DB 1; Length 136;  
Best Local Similarity 72.1%; Pred. No. 7.3e-45;  
Matches 98; Conservative 14; Mismatches 23; Indels 1; Gaps 1;

```

QY 1 MGNMCIFFLVTTATGVHSQVQVQSGAEYKRRSSRYKVCCKSGYFTFYAIAOWVQAP 60
   |||:||||| |||:||||| |||: |||: |||: |||: |||: |||: |||: |||:
DB 1 MGNMCIFFLVTTATGVHSQVQVQSGAEYKRRSSRYKVCCKSGYFTFYAIAOWVQSH 60
   |||:||||| |||:||||| |||: |||: |||: |||: |||: |||: |||:
QY 61 GGGEWIGVINYIDNNYNQKFKGKATMTVDKSTSAVYKELSLRSEDDAVVYCAR-AA 119
   : |||||: | ||:||||| |||||: |||||: |||||: |||||: |||||: |||||:
DB 61 AKSLIEWIGVISTNGNTSYNQKFKGKATMTVDKSSSTIVHMLRLTSDSANLYCARYG 120

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QY 120 WYMDYWGQGLTVYSS 135  
 DB 121 NYFDYWGQGLTVYSS 136

RESULT 2

HV07\_MOUSE STANDARD; PRT; 139 AA.  
 ID HV07\_MOUSE  
 AC P01751; P01752;  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 heavy chain V region B1-8/186-2 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
 CC -----  
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 CC -----  
 CC EMBL: J00529; AAA38170.1; -  
 CC PIR: A02034; MIMSI8.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC Pfam: PF00047; Ig\_V.  
 CC SMART: SM00406; IgV\_1.  
 CC KMW Immunoglobulin V region; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.  
 CC FT DOMAIN 20 49 FRAMEWORK-1.  
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 CC FT DOMAIN 55 54 FRAMEWORK-2.  
 CC FT DOMAIN 69 68 COMPLEMENTARITY-DETERMINING-2.  
 CC FT DOMAIN 86 117 FRAMEWORK-3.  
 CC FT DOMAIN 118 122 D SEGMENT.  
 CC FT DISULFID 41 115 JH2 SEGMENT.  
 CC FT NON\_TER 137 137 BY SIMILARITY.  
 CC SEQUENCE 139 AA; 15419 MW; 1B57D4FDD0C9F465 CRC64;

QY 120 WYMDYWGQGLTVYSS 135  
 DB 121 NYFDYWGQGLTVYSS 136

Query Match 69.6%; Score 501; DB 1; Length 139;  
 Best Local Similarity 68.3%; Pred. No. 1.4e-43;  
 Matches 95; Conservative 16; Mismatches 24; Indels 4; Gaps 1;

QY 1 MGNCIIFLVATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIAOWVQAP 60  
 DB 1 MGNSCIMFLAATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIAOWVQAP 60  
 QY 61 GGLGIEWIGINITYDNTNYYNOKFRKATMTVDKSTAYVWELSLRSEDYAVYYCAR-- 117  
 DB 61 GGLGIEWIGRIDPNVSGGTYYNHFRRSKATLTITDKPSSYAYWQLSLSEDSAVYYCARVDY 120  
 QY 118 -AAYMDYWGQGLTVYSS 135  
 DB 121 NYFDYWGQGLTVYSS 136

DB 121 YGSSYFDYWGQGLTVYSS 139

RESULT 3

HV11\_MOUSE STANDARD; PRT; 137 AA.  
 ID HV11\_MOUSE  
 AC P01755;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 19 heavy chain V region S43 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPB family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA  
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL  
 CC (NPB ANTIBODIES).  
 CC -----  
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 CC -----  
 CC EMBL: J00539; AAA38172.1; -  
 CC PIR: A02038; GZMS43.  
 CC InterPro: IPR003006; Ig\_MHC.  
 CC Pfam: PF00047; Ig\_V.  
 CC SMART: SM00406; IgV\_1.  
 CC KMW Immunoglobulin V region; Signal.  
 CC FT SIGNAL 1 19  
 CC FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.  
 CC FT DOMAIN 20 49 FRAMEWORK-1.  
 CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
 CC FT DOMAIN 55 54 FRAMEWORK-2.  
 CC FT DOMAIN 69 68 COMPLEMENTARITY-DETERMINING-2.  
 CC FT DOMAIN 86 117 FRAMEWORK-3.  
 CC FT DOMAIN 118 122 D SEGMENT.  
 CC FT DISULFID 41 115 JH2 SEGMENT.  
 CC FT NON\_TER 137 137 BY SIMILARITY.  
 CC SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 67.8%; Score 488; DB 1; Length 137;  
 Best Local Similarity 67.2%; Pred. No. 2.7e-42;  
 Matches 92; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 1 MGNCIIFLVATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIAOWVQAP 60  
 DB 1 MGNSCIMFLAATATGVSVOLOVSGAEVKKPGSSVYKSCASGYFTFYAIAOWVQAP 60  
 QY 61 GGLGIEWIGINITYDNTNYYNOKFRKATMTVDKSTAYVWELSLRSEDYAVYYCAR--RA 118  
 DB 61 GGLGIEWIGRIDPNVSGGTYYNHFRRSKATLTITDKPSSYAYWQLSLSEDSAVYYCARYL 120  
 QY 119 AAYMDYWGQGLTVYSS 135  
 DB 121 NYFDYWGQGLTVYSS 136

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RESULT 4
HV48_MOUSE STANDARD: PRT: 138 AA.
AC P03980:
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RT Tucker P.W.;
RT "illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma."
Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15376 MW; 748157E4C6907B8E CRC64;

Query Match 67.7%; Score 487.5; DB 1; Length 138;
Best Local Similarity 68.8%; Pred. No. 3, 1e-42;
Matches 95; Conservative 16; Mismatches 24; Indels 3; Gaps 1;

OY 1 MGNWNCIFLVTTATGVSQVQLVQSGAEVKKRPGSSVKVSKCASKAGTFTDYAIGWRAP 60
DB 1 MGNSTIIFLVATARDVHSQVQLQPGAEIVKPGASVQLSCASGHTFTNWMYHWKORP 60
OY 61 GGGLEWIGVINIYDNTNNTNOKFKKATMTVDKSTAMELSSLRSEPTAYVYCARAAW 120
DB 61 GGGLEWIGELINFGDRSNYNEKFKKATLTVDKSSSTAYMQLSLPEEFAYVYCARSDG 120
OY 121 YMD---YWGOGTLTVSS 135
DB 121 YMDVYVWGOGTLTVFSA 138

RESULT 5
HV02_MOUSE STANDARD: PRT: 140 AA.
AC P01746:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 9367 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-A/J;
RX MEDLINE=82152818; PubMed=6801765;

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RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -----
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CC -----
CC EMBL: J00493; AAA38128.1; -.
DR PIR: A02028; HVMST7.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Antiarsonate antibody; HydrIdoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 67.2%; Score 483.5; DB 1; Length 140;
Best Local Similarity 65.7%; Pred. No. 7, 9e-42;
Matches 92; Conservative 17; Mismatches 26; Indels 5; Gaps 1;

OY 1 MGNWNCIFLVTTATGVSQVQLVQSGAEVKKRPGSSVKVSKCASKAGTFTDYAIGWRAP 60
DB 1 MGNSTIIFLVTTATGVSQVQLQPGAEIVKPGASVQLSCASGHTFTNWMYHWKORP 60
OY 61 GGGLEWIGVINIYDNTNNTNOKFKKATMTVDKSTAMELSSLRSEPTAYVYCARAAW 120
DB 61 GGGLEWIGVINIYDNTNNTNOKFKKATMTVDKSTAMELSSLRSEPTAYVYCARSHY 120
OY 121 Y-----MDYWGOGTLTVSS 135
DB 121 YGGSYFDYWGOGTPIVSS 140

RESULT 6
HV06_MOUSE STANDARD: PRT: 117 AA.
AC P01750:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GENE LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NRB ANTIBODIES.
CC PIR: A02033; HVMST2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Signal.

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[illegible]

SEQUENCE	117 AA;	13016 MW;	427C861C53975EDC	CRC64;
Query Match	64.3%;	Score 463;	DB 1;	Length 117;
Best Local Similarity	75.6%;	Pred. No. 7.4e-40;		
Matches 90;	Conservative 12;	Mismatches 13;	Indels 4;	Gaps 2;
QY	1	MGMNCTIFFLVATGAVHSOVOLVOSGAEVKKPGSSVYVSCASGTFETDAIOWROAP	60	
DB	1	MGMSCTILFLVATGAVHSOVOLVOPGAEVLPRGSSVYKLSKASGTYTTSTYMDWVKRQRP	60	
QY	61	GQGLEMIGVINYNTNTYNQKFKKATMTVDKSTSTAYMELSLRSEDYAVYYCAR	117	
DB	61	GQGLEMIGVINYNTNTYNQKFKKATMTVDKSTSTAYMELSLRSEDYAVYYCAR	117	
RESULT	8			
AC	HYV4_MOUSE	STANDARD;	PRT;	117 AA.
AC	P01748;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V region 23 precursor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;			
RX	MEDLINE=81234548; PubMed=6788376;			
RA	Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajeswsky K.,			
RA	Baltimore D.;			
RT	"Heavy chain variable region contribution to the NpB family of			
RT	antibodies: somatic mutation evident in a gamma 2a variable region.";			
CC	Cell 24:625-637(1981).			
CC	-I- MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY			
CC	RELATED GENES, THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.			
DR	PIR: A02030; HVMS23.			
DR	InterPro: IPR003006; IG-MHC.			
DR	InterPro: IPR003596; IG_V.			
DR	Pfam: PF00047; Ig: 1.			
DR	SMART: SM00406; IgV: 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL	1	19	
FT	CHAIN	20	117	IG HEAVY CHAIN V REGION 23.
FT	DOMAIN	20	49	FRAMEWORK-1.
FT	DOMAIN	50	54	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	55	68	FRAMEWORK-2.
FT	DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	86	117	FRAMEWORK-3.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON_TER	117	117	
SEQUENCE	117 AA;	12772 MW;	C530F829C906F69B	CRC64;
Query Match	62.1%;	Score 447;	DB 1;	Length 117;
Best Local Similarity	71.8%;	Pred. No. 3e-38;		
Matches 84;	Conservative 11;	Mismatches 22;	Indels 0;	Gaps 0;
QY	1	MGMNCTIFFLVATGAVHSOVOLVOSGAEVKKPGSSVYVSCASGTFETDAIOWROAP	60	
DB	1	MGMSCTILFLVATGAVHSOVOLVOPGAEVLPRGSSVYKLSKASGTYTTSTYMDWVKRQRP	60	
QY	61	GQGLEMIGVINYNTNTYNQKFKKATMTVDKSTSTAYMELSLRSEDYAVYYCAR	117	
DB	61	GQGLEMIGVINYNTNTYNQKFKKATMTVDKSTSTAYMELSLRSEDYAVYYCAR	117	
RESULT	9			
ID	HYV1B_HUMAN	STANDARD;	PRT;	117 AA.

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AC P01743:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-I region H3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups.";
RC Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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CC -----
DR EMBL: J00240; AA552988.1; -
DR PIR: A02024; HVH0HG.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN
FT NON_TER
FT SEQUENCE
SQ
Query Match
Best Local Similarity 61.7%; Score 444; DB 1; Length 117;
Matches 85; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

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RA Bemmich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC - MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR: A02026; E1HUND.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN
FT MOD_RES
FT DISULFID
FT CONFLICT
FT CONFLICT
FT CONFLICT
FT NON_TER
FT SEQUENCE
SQ
Query Match
Best Local Similarity 59.2%; Score 444; DB 1; Length 147;
Matches 87; Conservative 17; Mismatches 31; Indels 12; Gaps 1;

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QY 1 MGNWCIIFLYTTATGVHSGVQVLOSAGAEVKKRGSVKYSCASGYTFDYAIQWRQAP 60
DB 1 MDTWXXHFLVAAATRVHSGTQVLOSAGAEVKKRGSVKYSCASGYTFDYAIQWRQAP 60
QY 61 GGLLEWIGVINIYDNTNNGKFKGKATMTVDKSTAYMELSLSEPTAYVYCAR-- 118
DB 61 GGLLEWIGVINIYDNTNNGKFKGKATMTVDKSTAYMELSLSEPTAYVYCAR 120
QY 119 -----AMTYDYWGQGLTVTVSS 135
DB 121 FMSDYNYFPDYSTYLDWAGQGLTVTVSS 147
RESULT 11
HVO9_MOUSE
ID HVO9_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RC MEDLINE=8134548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:625-637(1981).
CC - MISCELLANEOUS: THIS GERM LINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR: B02034; HVMS61.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL
FT CHAIN
FT SEQUENCE
SQ
Query Match
Best Local Similarity 61.7%; Score 444; DB 1; Length 147;
Matches 87; Conservative 17; Mismatches 31; Indels 12; Gaps 1;

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FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12890 MW; 16191A08CB17F5A CRC64;

Query Match 61.0%; Score 439; DB 1; Length 117;  
Best Local Similarity 70.1%; Pred. No. 1.9e-37;  
Matches 82; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

OY 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
DB 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
OY 61 GQGLEWIGVINYDNTNOKFKGKATMTVDKSTSTAYMELSLRSEDTAVYYCAR 117  
DB 61 GQGLEWIGRIDPNSSGCTKYNEKFKSKATLTVDPSSTAYMQLSLRSEDSAVYYCAR 117

## RESULT 12

HLVIG\_HUMAN STANDARD; PRT; 117 AA.  
AC P23083;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-I region V35 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88296408; PubMed=2841108;  
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.O.,  
RA Ohno H., Fukuhara S., Honjo T.;  
RT "Dispersed localization of D segments in the human immunoglobulin  
heavy-chain locus";  
RL EMBL J. 7:1047-1051(1988).  
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CC -----  
CC EMBL: X07448; NOT\_ANNOTATED\_CDS.  
DR PIR: S00476; HHVH35.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 61.0%; Score 439; DB 1; Length 117;  
Best Local Similarity 73.5%; Pred. No. 1.9e-37;  
Matches 86; Conservative 6; Mismatches 25; Indels 0; Gaps 0;

OY 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
DB 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60

OY 61 GQGLEWIGVINYDNTNOKFKGKATMTVDKSTSTAYMELSLRSEDTAVYYCAR 117  
DB 61 GQGLEWIGRIDPNSSGCTKYNEKFKSKATLTVDPSSTAYMQLSLRSEDSAVYYCAR 117

RESULT 13  
HLV49\_MOUSE STANDARD; PRT; 117 AA.  
AC P06328;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region VH558 B4 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85099340; PubMed=2578321;  
RA Yancopoulos G.D., Alt F.W.;  
RT "developmentally controlled and tissue-specific expression of  
RT unrearranged VH gene segments";  
RL Cell 40:271-281(1985).  
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CC -----  
CC EMBL: M13788; AAA38506.1; -  
DR PIR: A02035; MHMSB4.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IgV\_1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 60.4%; Score 435; DB 1; Length 117;  
Best Local Similarity 69.2%; Pred. No. 4.8e-37;  
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
DB 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
OY 61 GQGLEWIGVINYDNTNOKFKGKATMTVDKSTSTAYMELSLRSEDTAVYYCAR 117  
DB 61 GQGLEWIGRIDPNSSGCTKYNEKFKSKATLTVDPSSTAYMQLSLRSEDSAVYYCAR 117

RESULT 14  
HLV10\_MOUSE STANDARD; PRT; 117 AA.  
AC P01754; P11270;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region I45 precursor.

OY 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60  
DB 1 MGNWCIIFLVYTTATGVHSOVOLVOSGAEVKKPGSSVKVSKASGYTFDYAIQWYCAR 60

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: J00533; AAA8602.1; -
DR PIR: C02034; HVMS45.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 59.6%; Score 429; DB 1; Length 117;
Best Local Similarity 69.2%; Pred. No. 1.9e-36;
Matches 81; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

OY 1 MGNMCIIFLVTTATGVHQQVQVQGAEVKRGSSVKSCASGYTFDYAIQWVROAP 60
DB 1 MGNMCIIFLVTTATGVHQQVQVQGAELVYKPGASVKLSKASGYTFDYAIQWVROAP 60
OY 61 GGGLEMIQVINYDNTYNQKFKKATVVDKSTSTAYMELSLRSEDTAVYYCAR 117
DB 61 GGGLEMIQVINYDNTYNQKFKKATVVDKSTSTAYMELSLRSEDTAVYYCAR 117

RESULT 15
HVL3_MOUSE STANDARD; PRT; 117 AA.
ID HVL3_MOUSE
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765383;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
```

```

RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26242; MEMS75.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region.
FT DISUFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 59.4%; Score 427.5; DB 1; Length 117;
Best Local Similarity 70.1%; Pred. No. 2.7e-36;
Matches 82; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

OY 20 QVQLVQSGAEVKKRGSSVKSCASGYTFDYAIQWVROAPGGLEMIQVINYDNTYN 79
DB 1 EVQLOQSGPELVKPGASVKKSCASGYTFDYIMKWKQSHGKSLIEWIGDINPNNGCTSY 60
OY 80 NQKFKKATVVDKSTSTAYMELSLRSEDTAVYYCAR-AAATMDYWGQGLTVVSS 135
DB 61 NQKFKKATVVDKSSSTAYMOLNLSLSEDSAVYYCARDRRYWYFDWAGAGTVTVSS 117
```

Search completed: August 26, 2002, 15:05:39  
Job time: 358 sec







ID	AC	PRELIMINARY:	PRT:	473 AA.
DT	09DBL4			
DT	01-JUN-2001 (TEMBLrel. 17, Created)			
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)			
DE	1810060009RIK PROTEIN.			
GN	IGH-1 OR 1810060009RIK.			
OS	Mus musculus (mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=210855660; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Atakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Altzo K., Izawa M., Nishii K., Kiyosawa H., Kondo S., Yamana K. I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kodori C., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Glassi C., King B., Koehisa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirrm L.M., Staudt F., Suzuki K., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Giustolich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzaresli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Wiltaker C., Wilmink L.,			
RA	Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohitsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001)			
DR	EMBL; AK007918; BAB2549.1; -.			
DR	HSSP; P01842; 7FAB.			
DR	MGD; MGI:96443; Igh-1.			
DR	InterPro; IPR003597; Ig.			
DR	InterPro; IPR003597; Ig.cl.			
DR	InterPro; IPR003600; Ig_likc.			
DR	InterPro; IPR003006; Ig_LHHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_4.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00407; IGC1; 3.			
DR	SMART; SM00406; IGY; 1.			
DR	SMART; SM00410; IGLike; 1.			
DR	PROSITE; PS00290; IG_LHHC; UNKNOWN.1.			
DR	SEQUENCE 473 AA; 51699 MW; 9DED57A51475FBB CRC64;			

	Query Match	67.3%	Score 484.5:	DB 11:	Length 473;	
	Best Local Similarity	66.7%	Pred. No. 7.8e+41:			
	Matches	92;	Conservative	18;	Mismatches 25;	Indels 3; Gaps 1.
OY	1 MGWNCIEFLVTTATGVSHQVOLYOSGAELVKPGSSVKVSKASGTYFTDYAIIQWVRQAP	60				
	: :   : :   : :   : :   : :   : :   : :   : :					
Dd	1 MEMSVVFLLFSLVTAGVHCQVOLKSGAEILVPKGASIVKISCKASGYTFPTYIYNWKQRP	60				
OY	61 GGGLMEIGVINIYDNTNVNOKEGKAKMTVDKSTASTAMELTSRDEPTAYVYCARRAW	120				
Dd	61 GGGLMEICKIPGSGSYTIINEKFKKRAITLADKSSSTAIMQLSLSSEDSAVYFCARSET	120				
OY	121 YMD---YWGQGTLVTVSS	135				
Dd	121 DYDMFAFYMGQGTLYTVSA	138				
RESULT	3					
O9JWR1						
ID O9JWR1	PRELIMINARY;	PRT:	488 AA.			
MC O9JWR1;						

DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE HYPOTHETICAL 53.0 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N/A.  
RC TISSUE=KIDNEY; |  
RC Strausberg R.; |  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013539; AANH3539.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match	65.8%	Score 474	DB 11	Length 488
Best Local Similarity	62.2%	Pred. No. 9,3e-40		
Matches	89	Conservative	21	Mismatches 25; Indels 8; Gaps 1
QY	1	MGWNCIIFFLVTTATGVSQVQVLOSAGAEVRRKPGSSVKVSKASGTYTFTDVAIQWYRQAP	60	
DB	1	MGWNNIFELFSLGTAGISSEVQLOOSGPELVKPGASVKLSKASGTYITDYVVMWKOSH	60	
QY	61	GQGLEWIGIVINITYNTNPNOKFKGKATMTYDKSTATAMELSSLRSEPTAVYYCAR	120	
DB	61	GSLSEWIGIDINPGSTISNOKFKGKATLTVKSSIAIMQNLNLTSDSAVYYCAR	120	
QY	121	YMW-----DYWGQGLTVTVSS	135	
DB	121	YYSYFSYDRGDYWGQGLTVTVSA	143	
RESULT	4			
ID	Q91WT3	PRELIMINARY;	PRT;	481 AA.
AC	Q91WT3			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	HYPOTHEITICAL 52.0 kDa PROTEIN.			
DE	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=COLON;			
RA	Strausberg R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC013488; AAH13488.1; ..			
KW	Hypothetical protein.			
SO	SEQUENCE	481 AA;	52022 MW;	4EBB5C253038B718 CRC64;
Query Match	64.7%	Score 465.5	DB 11;	Length 481;
Best Local Similarity	66.2%	Pred. No. 6,7e-39;		
Matches	92	Conservative	19	Mismatches 21; Indels 7; Gaps 3
QY	1	MGWNCIIFFLVTTATGVSQVQVLOSAGAEVRRKPGSSVKVSKASGTYTFTDVAIQWYRQAP	60	
DB	1	MGWNNIFELFSLGTAGISSEVQLOOSGPELVKPGASVKLSKASGTYITDYVVMWKOSH	60	
QY	61	GQGLEWIGIVINITYNTNPNOKFKGKATMTYDKSTATAMELSSLRSEPTAVYYCAR	117	
DB	61	GQGLEWIGIADPDSYTSYNOKFKG-TLTVPTSSSAVYMLSLTSEDSAVYFCARGPR	119	
QY	118	AAATMDYWGQGLTVTVSS	135	
DB	120	DSSGY--YWGQGLTVTVSS	136	



[illegible]

RESULT	9			
099L25		PRELIMINARY:	PRT:	473 AA.
ID	099L25			
AC	099L25;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	SIMILAR TO RIKEN CDNA 1810060009 GENE.			
OC	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.			
RL	EMBL: BC003888; AAH03888.1; -			
DR	HSSP; P01842. 7FAB.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003597; Ig-cl.			
DR	InterPro; IPR003600; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig; 4.			
DR	SMART; SM00409; Ig; 2.			
DR	SMART; SM00407; IGc1; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	SMART; SM00410; IG_Like; 1.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN.1.			
SO	SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;			

	Query Match	63.8%	Cred. 459;	DB 11;	Length 473:
	Best Local Similarity	60.1%;	Pred. No. 3e-38;		
	Matches	86;	Conservative	20; Mismatches	29; Indels
					8; Gaps
Oy	1 MGWNCIEFFLVTTATQVHSHOVQLVSGAEVKRPGSSVKYSCRASGYTFDYALIQWVRQAP	60			
Dd	1 MEMSVWFLEFLFSLVTGTVHSHOVLQOSDDELAVPRGASVSKISCVSGYTFTDHTLIHWKCRP	60			
Oy	61 GGGLGMICIVINITYNTNPNOKCKRAFMPTVKKSTATAEMLSSLREEDTAYYYCARAA-	119			
Dd	61 EGGLMEMIGITIPRDGSTKNENFKGKAAILTLADKSSSTAAYMOLNSLTSEDSAVCFCSRGGS	120			
Oy	120 -----WMYDWYGQGTLEVTS	135			
Dd	121 IYKGGLVEFYFDYWGQTITVS	143			
RESULT	1C				
Q9BRV0					
ID Q9BRV0	PRELIMINARY;		PRT;	500 AA.	
AC Q9BRV0;					

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DT      01-JUN-2001 (TREMBLrel. 17, created)
DT      01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE      HYPOTHEETICAL 54.2| KDA PROTEIN.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606; |
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=PROSTATE; |
RA      Strausberg R.; |
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC005951; AAH05951.1; -.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003599; Ig_
DR      InterPro; IPR003597; Ig_cl.
DR      InterPro; IPR003600; Ig_like.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig_4.
DR      SMART; SM00409; Ig; 4.
DR      SMART; SM00407; Igcl; 2.
DR      SMART; SM00406; Igv; 1.
DR      SMART; SM00410; Ig_like; 1.
DR      PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW      Hypothetical protein.
SQ      SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

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Query Match	Best Local Similarity	Matches	63.2%	Score 455:	DB 4:	Length 500:
			Conservative	Pred. No. 8.1e-38:	Mismatches 32:	Indels 12:
						Gaps 1:
Qy	1	MGAMNCITFLVLTATGVHSQVOLVOSGAEEVKKPGSSVSVSCASGTFTEIDAIQWROAP	60			
Db	1	MDMTSILFLVAAATGAOSQVHLVOSGAEEVMSPGASVRSCTSOYAHHTYSIIWVRAP	60			
Qy	61	GGGLEMGIVINITYNTNYNOKFKKATWYVDKSTSTAYAMELISLRSEDTAVYYCARA--	118			
Db	61	GGGLEMGWISPSNTRFPAKKFGCRVLTLDSTSTVYMEILRSRSDPTAVYYCARRYC	120			
Qy	119	-----AMTMDYNGGGLTVTVSS	135			
Db	121	SYSSQANDYIYYIMDYMGKGTTVVSS	147			

RESULT	11		
ID	090U92	PRELIMINARY:	PRT: 124 AA.
AC	090U92:		
DT	01-MAY-2000	(TREMBLrel. 13, Created)	
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL: AF035022; AAD56258.1; -		
DR	HSSP: P01772; 2F84.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_v.		
DR	Pfam: PF00047; 19; 1.		





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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:57:46 ; Search time 42.03 Seconds

(without alignments)  
356.768 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720  
Sequence: 1 MGNMCIIFFLVTARGVHSQ.....AAAWMYDWGGLTVVSS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

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7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*

8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:\*

9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:\*

10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:\*

11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:\*

12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:\*

13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:\*

14: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:\*

15: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:\*

16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:\*

17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:\*

18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:\*

19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:\*

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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:\*

22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	135	21	AAAB07965
2	627	87.1	135	21	AAAB07963
3	585.5	81.3	470	21	AAAB09035
4	582.5	80.9	470	21	AAAB09033
5	581.5	80.8	470	21	AAAB09034
6	579.5	80.5	470	19	AAAB83037
7	579.5	80.5	470	21	AAAB14779
8	579.5	80.5	470	21	AAAB09029
9	573.5	79.7	140	15	AAAB55556
10	567.5	78.8	470	21	AAAB09036
11	566.5	78.7	145	19	AAAB83038

12	566.5	78.7	145	21	AAAB14775	Fragment of human
13	566.5	78.7	145	21	AAAB09025	Humanised anti-Fas
14	566.5	78.7	470	19	AAAB83036	Anti-Fas humanised
15	566.5	78.7	470	21	AAAB14776	Humanised anti-Fas
16	566.5	78.7	470	21	AAAB09026	Humanised HFE7A de
17	554	76.9	588	19	AAAB71880	Anti-human Fas hum
18	554	76.9	588	21	AAAB12917	Anti-human Fas imm
19	547	76.0	515	22	AAAB52162	Humanised HMG-1 F
20	547	76.0	517	22	AAAB52154	Humanised HMG-1 F
21	547	76.0	519	22	AAAB52164	Humanised HMG-1 F
22	547	76.0	519	22	AAAB52165	Humanised HMG-1 F
23	547	76.0	521	22	AAAB52163	Humanised HMG-1 F
24	547	76.0	525	22	AAAB52166	Humanised HMG-1 F
25	547	76.0	527	22	AAAB52155	Humanised HMG-1 F
26	547	76.0	529	22	AAAB52168	Humanised HMG-1 F
27	547	76.0	531	22	AAAB52167	Humanised HMG-1 F
28	547	76.0	729	22	AAAB52158	Humanised HMG-1 h
29	547	76.0	730	22	AAAB52157	Humanised HMG-1 h
30	547	76.0	731	22	AAAB52156	Humanised HMG-1 h
31	547	76.0	739	22	AAAB52161	Humanised HMG-1 h
32	547	76.0	740	22	AAAB52160	Humanised HMG-1 h
33	547	76.0	741	22	AAAB52159	Humanised HMG-1 h
34	546	75.8	135	13	AAAB24107	Humanised anti-Tac
35	545	75.7	135	11	AAAB06369	Humanised anti-Tac
36	545	75.7	135	22	AAAB69653	Humanised anti-Tac
37	541	75.1	461	22	AAAB72236	Humanised 323/A3 (
38	541	75.1	462	22	AAAB72229	Humanised 323/A3 (
39	541	75.1	462	22	AAAB72234	Humanised 323/A3 (
40	541	75.1	464	22	AAAB72232	Humanised 323/A3 (
41	541	75.1	465	22	AAAB72228	Humanised 323/A3 (
42	540	75.0	135	21	AAAB80289	Humanised anti-Fas
43	537	74.6	135	21	AAAB80288	Humanised anti-Fas
44	532	73.9	588	19	AAAB71881	Anti-human Fas hum
45	532	73.9	588	21	AAAB12918	Anti-human Fas imm

## ALIGNMENTS

RESULT 1	
AAAB07965	standard; Protein; 135 AA.
ID	AAAB07965;
AC	AAAB07965;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	A heavy chain variable region of humanised 3S1 antibody.
XX	
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulin; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Peptide 1..19
FT	/note- "signal peptide"
FT	Protein 20..135
FT	/note- "mature protein"
FT	Region 50..54
FT	/note- "complementarity determining region 1"
FT	Region 69..85
FT	/note- "complementarity determining region 2"
FT	Region 118..124
FT	/note- "complementarity determining region 3"
XX	

PN W0200047625-A2.  
 XX 17-AUG-2000.  
 XX  
 XX 09-FEB-2000; 2000MO-US03303.  
 XX  
 XX 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 XX (GEMV ) GENETICS INST INC.  
 PA Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 XX WPI: 2000-524532/47.  
 DR N-PSDB; AAA59694.  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 PS Example 3; Fig 2A; 162pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region  
 CC of the humanised murine antibody 3D1. The antibody has a binding  
 CC specificity to B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX Sequence 135 AA;  
 SQ  
 Query Match 100.0%; Score 720; DB 21; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-55;  
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGNMCIFFLVTTATGHSOVQLVQSGAEVKKPGSSVSKVSCSKASGYFTFDYAIQWVQAP 60  
 DB 1 mgnmciiffvlvtatgshsqvqlvqsgaevkkpgssvskvscskasgyftfdyaigwvqap 60  
 QY 61 GGGLEWIGVINIYYDNTNMYNOKFKGKATWVDKSTAYWELSSLRSEDTAVVYCARAAW 120  
 DB 61 ggglewigviniiyydntnmynokfkgkatwvdkstaywelslsrsedevvycaraaw 120  
 QY 121 YMDYWGQGLTVTVSS 135  
 DB 121 ymdywgqgltlvss 135  
 RESULT 2  
 AAB07963  
 ID AAB07963 standard; Protein; 135 AA.  
 AC AAB07963;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Amino acid sequence of heavy chain variable region of 3S1 antibody.  
 XX  
 XX Antibody 3D1: B7 molecule; B7: humanised immunoglobulin;  
 KM autoimmune disease; infectious disease; inflammatory disorder;  
 KM systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;  
 KM arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;

KM multiple sclerosis; transplant rejection; proliferative disease;  
 KM leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;  
 KM aplastic anaemia; myeloid dysplasia syndrome.  
 XX  
 XX Mus sp.  
 OS  
 XX  
 XX Key  
 FH Peptide  
 FT  
 FT Protein  
 FT  
 FT Region  
 FT Region  
 FT Region  
 FT Region  
 FT Region  
 FT Region  
 XX W0200047625-A2.  
 XX 17-AUG-2000.  
 XX  
 XX 09-FEB-2000; 2000MO-US03303.  
 XX  
 XX 12-FEB-1999; 99US-0249011.  
 PR 24-JUN-1999; 99US-0339596.  
 XX  
 XX (GEMV ) GENETICS INST INC.  
 PA Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 XX WPI: 2000-524532/47.  
 DR N-PSDB; AAA59692;  
 XX  
 XX Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 PS Example 1; Fig 1A; 162pp; English.  
 XX  
 CC The present sequence represents the heavy chain variable region of the  
 CC murine antibody 3D1. The antibody has a binding specificity to B7  
 CC molecules. The antibody is used to construct humanized immunoglobulins,  
 CC which comprise an antigen binding region of non-human origin and a  
 CC portion of a human immunoglobulin. The humanized immunoglobulins are  
 CC useful for treating autoimmune diseases, infectious diseases,  
 CC inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient or preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 CC  
 XX Sequence 135 AA;  
 SQ  
 Query Match 87.1%; Score 627; DB 21; Length 135;  
 Best Local Similarity 84.4%; Pred. No. 4.0e-47;  
 Matches 114; Conservative 10; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MGNMCIFFLVTTATGHSOVQLVQSGAEVKKPGSSVSKVSCSKASGYFTFDYAIQWVQAP 60  
 DB 1 mgnmciiffvlvtatgshsqvqlvqsgaevkkpgssvskvscskasgyftfdyaigwvqsh 60  
 QY 61 GGGLEWIGVINIYYDNTNMYNOKFKGKATWVDKSTAYWELSSLRSEDTAVVYCARAAW 120  
 DB 61 akslewigviniiyydntnmynokfkgkatwvdkstssstaywelslsrsedevvycaraaw 120  
 QY 121 YMDYWGQGLTVTVSS 135



Db 121 ymdywgqglvtvss 135

## RESULT 3

AAW90935 standard; protein; 470 AA.

AAW90935;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 3 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP90663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB; AAA11646.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 180-182; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antinfertility, neuroprotective, antarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (inulant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic

CC the native ligand, do not induce liver disease, and have reduced risk of CC inducing a human anti-murine antibody response. This sequence represents CC a humanised anti-Fas antibody heavy chain construct designated Heu 3 CC which is described in the method of the invention.

SO Sequence 470 AA;

Query Match 81.3%; Score 585.5; DB 21; Length 470;  
Best Local Similarity 81.4%; Pred. No. 6,7e-43;  
Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 1;

0y 1 MGNACIIFLVTTATGCHSOVQLVQSGAEVKKPGSSSVVSKASGYTFTDIAIQWVRAP 60

Db 1 mgwscilflfvalatgysqvqlvqsgaevkkpgasvkskasgyltfsymwqwrqap 60

0y 61 GGGLEWGVINIIYDNTNMYNOKFKGATMTYDKNSTAYMELSSRSDDTAVVYCARAA- 119

Db 61 99glewmgelopsdsytnqkfkqkalcitvdstustaymelslrseddavyycaarnrd 120

0y 120 ---WYMDYWGQGLVTVSS 135

Db 121 ysmwyfdvwwgqglvtvss 140

## RESULT 4

AAW90933 standard; protein; 470 AA.

AAW90933;

08-AUG-2000 (first entry)

Humanised anti-Fas designed heavy chain Heu 1 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hepatotropic; antinfertility; neuroprotective; antarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP90663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

WPI: 2000-258930/23.

N-PSDB; AAA11644.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 169-170; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephroprotective, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Hen 1  
 CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 80.9%; Score 582.5; DB 21; Length 470;  
 Best Local Similarity 80.7%; Pred. No. 1.2e-42;  
 Matches 113; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGWNCIIFLVTTATGHSQVQVQSGAEVKKPGSSVSKVSCASGYFTTDAIOMVROAP 60  
 Db 1 mgsccillflvatatgshgsgqlvsgaevkkgpasvskvscasytftsywmqvwkqap 60  
 QY 61 GQGLEWIGVINIYDNTMYNOKFKGKATMTVDKSTAYMELSSLRSEDTPVYYCARAA- 119  
 Db 61 gqglewmgeldpsdsytnqgkfkqkattlvdststajmelslrsedatavycarnrd 120  
 QY 120 ----WYMDYMGQGTLYTVSS 135  
 Db 121 ysmnwyfdvsgqglvtvss 140

RESULT 5

AAW90934  
 ID AAW90934 standard; Protein: 470 AA.

AC AAW90934;  
 DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas designed heavy chain Hen 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KM anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KM dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KM nephroprotective; antifertility; neuroprotective; antarteriosclerotic;  
 KM hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KM Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KM Sjorgen's syndrome; Addison's disease; scleroderma; sterility;  
 KM Goodpasture syndrome; Crohn's disease; myasthenia gravis;  
 KM multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KM cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.  
 OS EP990663-A2.  
 PN  
 XX  
 PD 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.  
 XX 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI: 2000-256930/23.  
 DR N-PSDB: AAA11645.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX Claim 2; Page 174-176; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephroprotective, antifertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Hen 2  
 CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 80.8%; Score 581.5; DB 21; Length 470;  
 Best Local Similarity 80.7%; Pred. No. 1.5e-42;  
 Matches 113; Conservative 7; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGWNCIIFLVTTATGHSQVQVQSGAEVKKPGSSVSKVSCASGYFTTDAIOMVROAP 60  
 Db 1 mgsccillflvatatgshgsgqlvsgaevkkgpasvskvscasytftsywmqvwkqap 60  
 QY 61 GQGLEWIGVINIYDNTMYNOKFKGKATMTVDKSTAYMELSSLRSEDTPVYYCARAA- 119  
 Db 61 gqglewmgeldpsdsytnqgkfkqkattlvdststajmelslrsedatavycarnrd 120  
 QY 120 ----WYMDYMGQGTLYTVSS 135  
 Db 121 ysmnwyfdvsgqglvtvss 140

RESULT 6  
 AAW83037  
 ID AAW83037 standard; Protein: 470 AA.  
 AC AAW83037;  
 XX



CC The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDS  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14775-814776 and AAB14779  
 CC represent the heavy chains (or fragments thereof) of various humanised  
 CC HFE7A-derived anti-Fas antibodies.  
 XX  
 SQ Sequence 470 AA;

Query Match 80.5%; Score 579.5; DB 21; Length 470;  
 Best Local Similarity 80.0%; Pred. No. 2.2e-42;  
 Matches 112; Conservative. 8; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGNMCIFFLVTTATGVSQVQLVQSGAEVKKRPPSSVYKSCASGYRTTDAIQWRQAP 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 1 mgsceillflvalatatyhsqqlvqsgaevkpkgsavsvckasgyrtfitymwmvkvqap 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 61 GQGLEWIGVINIYDNTNRYNOKFKGKATMYDKSTFAYMELSSLRSDTAVYYCARAA- 119  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 61 qgglewmgeldpsdyslyngkfkgkcltldtstststamelslrsdeltavyycaarnrd 120  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 120 ---WYMDYWGQGLTVTVSS 135  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 121 ysmnyfdwvgeglvtvss 140  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8  
 AAM90929  
 ID AAM90929 standard; Protein: 470 AA.  
 XX  
 AC AAM90929;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised HFE7A designed heavy chain protein #2.  
 XX  
 KW Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; anti-rheumatic; anti-Fas;  
 KW nephrotoxic; antileptile; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98UP-0276881.  
 PR 30-SEP-1998; 98UP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 PI Setizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI: 2000-258930/23.

DR N-PSDB: AAA11622.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX  
 PS Example reference 22; Page 150-152; 263pp; English.  
 XX  
 SS This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotoxic, antileptile, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
 CC the method described in the invention.  
 XX  
 SQ Sequence 470 AA;

Query Match 80.5%; Score 579.5; DB 21; Length 470;  
 Best Local Similarity 80.0%; Pred. No. 2.2e-42;  
 Matches 112; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 1 MGNMCIFFLVTTATGVSQVQLVQSGAEVKKRPPSSVYKSCASGYRTTDAIQWRQAP 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 1 mgsceillflvalatatyhsqqlvqsgaevkpkgsavsvckasgyrtfitymwmvkvqap 60  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 61 GQGLEWIGVINIYDNTNRYNOKFKGKATMYDKSTFAYMELSSLRSDTAVYYCARAA- 119  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 61 qgglewmgeldpsdyslyngkfkgkcltldtstststamelslrsdeltavyycaarnrd 120  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 QY 120 ---WYMDYWGQGLTVTVSS 135  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
 Db 121 ysmnyfdwvgeglvtvss 140  
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9  
 AAR55556  
 ID AAR55556 standard; Protein: 140 AA.  
 XX  
 AC AAR55556;  
 XX  
 DT 16-NOV-1994 (first entry)  
 XX  
 DE DRBG-200 Humanized antibody heavy chain variable region.  
 XX  
 KW DRBG-200; L-selectin; LECAM-1; Mel-14; LAM-1;  
 KW humanized antibody; immunoglobulin; Ig; IgG1; IgG4;  
 KW complementarity determining region; CDR; monoclonal antibody; Mab;  
 KW framework; light chain; heavy chain; variable domain;  
 KW monoclonal antibody; acceptor antibody Bu; transgenic animal.  
 XX  
 OS Mus sp.; Homo sapiens.

[illegible]

KW Fas; allergic; human; anti-inflammatory; anti-anemic; antidiabetic;  
KM anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thyromimetic; antihematic; anti-Fas;  
KM neoprotropic; antifertility; neuroprotective; antileukocytic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KM Hashimoto syndrome; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; Addison's disease; scleroderma; sterility;  
KM Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
OS Synthetic.  
XX  
XX  
PN EP990663-A2.  
XX  
PD 05-APR-2000.  
XX  
PF 29-SEP-1999; 99EP-0307711.  
XX  
PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX  
PA (SANY ) SANKYO CO LTD.  
PI Setizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
DR WPI: 2000-258930/23.  
XX N-PEDB; MAAL1655.  
XX  
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PR cells with abnormal Fas-Fas ligand systems -  
PS  
XX Claim 2; Page 188-189; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, neoprotropic, antifertility, neuroprotective,  
CC antileukotrophic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFEA heavy chain construct HHH type  
CC which is described in the method of the invention.  
XX  
SQ Sequence 470 AA;

Query Match 78.8%; Score 567.5; DB 21; Length 470;  
Best Local Similarity 78.6%; Pred. No. 2.4e-41;  
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

1 MGNMNTIFFLVYTAAGVSQVOLVDSGAEEKPPGSSVKVSKCAASGTTFDVAIDQWRAP 60

Db	1	mgwsc111flvatalatvhsqvgqlvqsgaevkvkpgasvkvsckaagylftysmqwvrvqap	60
Qy	61	GQGLEWIVINIIYDNTNYNOKFKGATMYDKSTSPAINELSLRESDPAVYCARAA-	119
Db	61	ggglewmge1pspsdytrngkfkygrvltirdtstslaymelslrsedlavycarnrd	120
Qy	120	---WYNDYWGQGLVTVVSS 135	
Db	121	ysnmwfgdwgegtlvrvss 140	
	RESULT 11		
ID	AAW83038		
AC	AAW83038 standard; Protein: 145 AA.		
XX	AAW83038;		
DT	15-MAR-1999 (first entry)		
XX			
DE	Anti-Fas humanised antibody HFE7A heavy chain variable region.		
XX			
KW	HE7A: monoclonal antibody; mouse; Fas; humanised antibody;		
KW	apoptosis; HE7A: autoimmune disease; Hashimoto's disease;		
KW	systemic lupus erythematosus; graft versus host disease;		
KW	Sjogren syndrome; pernicious anaemia; Addison's disease;		
KW	sceleroderma; Goodpasture syndrome; Crohn's disease; sterility;		
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;		
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;		
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;		
KW	atopy; arteriosclerosis; myocarditis; cardiomyopathy;		
KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;		
KW	transplant rejection; therapy.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/label= sig_peptide	
FT	Protein	20..145	
FT		/label= Mat_protein	
FT	Region	50..54	
FT		/label= CDR_H1	
FT		/note= "claim 9"	
FT	Region	69..84	
FT		/label= CDR_H2	
FT		/note= "claim 9"	
FT	Region	118..129	
FT		/label= CDR_H3	
FT		/note= "claim 9"	
XX			
XX	AU9835701-A.		
PN			
XX			
DD	08-OCT-1998.		
XX			
PE	30-MAR-1998;	98AU-0059701.	
XX			
XX			
PR	08-OCT-1997;	97JP-0276064.	
PR	01-APR-1997;	97JP-0082953.	
PR	25-JUN-1997;	97JP-0169088.	
XX			
PA	(SANY ) SANKYO CO LTD.		
XX			
PI	Akko S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;		
PI	Masahiko O, Nobutusa S, Shin Y, Tohru T;		
DR	WPI: 1998-543440/47.		
DR	N-PSDB: AAV70104.		
PT	New antibodies and proteins bind conserved epitope of Fas antigen -		
PT	used to evaluate drugs in animal models and to treat Fas-associated		
PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,		
PT	myocarditis, hepatitis and AIDS		

XX Example 3: Page|207; 292pp; English.

XX This is the amino acid sequence of the VD type humanised heavy

CC chain variable region of murine anti-human Fas monoclonal antibody

CC HFE7A. It was utilised in a claimed humanised HFE7A heavy chain

CC (see AAV70079). The invention provides methods for producing humanised

CC antibodies by culturing host cells. Humanised versions of HFE7A (see

CC AAW3031-37) are capable of inducing apoptosis in abnormal cells

CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal

CC cells. Humanised antibodies are used to evaluate, in animal models,

CC treatments of diseases that involve Fas/Fas ligand interactions, and

CC also to treat such diseases, including autoimmune disease (e.g.

CC systemic lupus erythematosus, Hashimoto's disease, graft versus host

CC disease, Sjogren syndrome, pernicious anaemia, Addison's disease,

CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid

CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia

CC gravis, multiple sclerosis, Basedow's disease, thrombocytopenic purpura

CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,

CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic

CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).

XX Sequence 145 AA:

SQL

Query Match 78.7%; Score 566.5; DB 19; Length 145;

Best Local Similarity 78.6%; Pred. No. 8.6e-42;

Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1.

QY 1 MGNMCIIFLVTTATGWSOVOLVDSGAERKPGSSVKVSKASGTTFTDAIOWRQAP 60

DB 1 MGVSCILIFLVATAGVHSQVGLVSGAEVKKPGASVKVSCKASGYLFTSYWYQVKKQP 60

QY 61 GGGLEMGIVNTIYNDNTNNOKFKGATFTVVKSTSTAYMELSLRSEPTAVYCARAA- 119

DB 61 GGLFMGSLGDSGYTNGKFKGKALIVTSSSTAYMELSLRSEDATVYCAARNR 120

QY 120 ---WYMDYWGQGITLVTVSS 135

DB 121 YSNWYFDWVGEGILTVTS 140

RESULT 12

AA14775 |

ID AAB14775 standard; peptide; 145 AA.

XX AC AAB14775; |

XX DT 24-NOV-2000 (first entry)

DE Fragment of humanised anti-Fas antibody heavy chain, SEQ ID NO:75.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

CC murine; humanised antibody; complementarity determining region; CDR;

CC human Fas; Fas ligand; apoptosis modulator; programmed cell death;

CC autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

CC cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

CC hepatitis; AIDS; graft rejection; heavy chain.

XX Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX JP2000169393-A.

XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.

XX 30-SEP-1998; 98JP-0276883.

XX (SANY ) SANKYO CO LTD.

XX WPI; 2000-485645/43.

[illegible]

PR	30-SEP-1998;	98JP-0276881.	
PR	30-SEP-1998;	98JP-0276882.	
PA	(SANY ) SANKYO CO LTD.		
PI	Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;		
DR	WPI: 2000-258930/23.		
DR	N-PSDB: AAA11584.		
PT	New humanized anti-Fas antibody, useful for treating or preventing e.g.		
PT	inflammatory or autoimmune disease, induces apoptosis selectively in		
PT	cells with abnormal Fas-Fas ligand systems		
PS	Example reference 15; Page 126-127; 263pp; English.		
XX	This invention describes a novel humanized anti-Fas antibody-like		
CC	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas		
CC	ligand system, by binding to Fas on the cell surface, and prevents		
CC	apoptosis in cells with a normal system, by inhibiting binding between		
CC	Fas and its ligand. The products of the invention have anti-inflammatory,		
CC	anti-neuritic, antidiabetic, anti-allergic, anti-arthritis, antiviral,		
CC	immunomodulatory, dermatological, immunosuppressive, thyromimetic,		
CC	antirheumatic, nephroprotective, antifertility, neuroprotective,		
CC	antiatherosclerotic, cardiact and hepatotropic activity. (I) induce		
CC	apoptosis by binding to cell surface Fas or inhibit it by competitive		
CC	inhibition of ligand binding. (I) are used to treat and/or prevent		
CC	diseases associated with the Fas/Fas ligand system, especially systemic		
CC	lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft		
CC	versus host disease, Sjorgen's syndrome, perniciolous or hypoplastic		
CC	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's		
CC	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,		
CC	multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin		
CC	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,		
CC	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral		
CC	(B, C or D) or alcoholic), and transplant rejection. (I) selectively		
CC	inhibit apoptosis in normal cells but selectively induce it in abnormal		
CC	cells. They bind to both human and murine Fas, so can be evaluated in		
CC	murine disease models. (I) act on the active site of Fas, i.e. they mimic		
CC	the native ligand, do not induce liver disease, and have reduced risk of		
CC	inducing a human anti-murine antibody response. This sequence represents		
CC	a humanised anti-Fas antibody HFE7A heavy chain which is used in		
CC	the method described in the invention.		
XX			
SQ	Sequence 145 AA;		
Query Match	78.7%; Score 566.5; DB 21; Length 145;		
Best Local Similarity	78.6%; Pred. No. 8.6e-42;		
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;			
QY	1 MGNMCTIFELVTATGCHISOVLQVDSGAEVKKPGSSVAVSCASGYTTTDAIQVRYAP 60		
db	1 mgscttllflvatagvhsqqlvsgaevkpkpgasvsvscasytlftsymgmwkvk 60		
QY	61 GGGLEWICIVININYYDNTYNNOKFKGKAMTYDKSSTRYMELTSSRSDDTVVYCARAA- 119		
db	61 gqrlewmgeiopsdasytrynqkfkxkalitvdtcsastaymelslrscdtavaycarnrd 120		
QY	120 ----WYMDYWGQGLTVTVSS 135		
db	121 ysmnwyfdwgegltlvtvss 140		
RESULT 14			
AAW83036			
ID	AAW83036 standard; Protein: 470 AA.		
AC	AAW83036;		
XX	15-MAR-1999 (first entry)		
XX	Anti-Fas humanised antibody HFE7A heavy chain.		

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Sig\_peptide  
 FT Protein 20..470  
 FT /label= Mat\_protein  
 FT Region 20..140  
 FT /label= Variable  
 FT Region 141..464  
 FT /label= Constant  
 FT Region 50..54  
 FT /label= CDR\_H1  
 FT /note= "claim 9"  
 FT Region 69..84  
 FT /label= CDR\_H2  
 FT /note= "claim 9"  
 FT Region 118..129  
 FT /label= CDR\_H3  
 FT /note= "claim 9"  
 XX  
 PN A09859701-A.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98AU-0059701.  
 PR 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 PI Akiro S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Toku T;  
 DR WPI: 1998-543440/47.  
 DR N-PSDB; AAV70079.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 22; Page 212-213; 292pp; English.  
 CC This is the amino acid sequence of the VD type humanised heavy  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
 CC pGSL7A62 SANK 73397 harbors plasmid pGSL7A62 carrying a fusion  
 CC fragment of the humanised VD type HFE7A heavy chain and DNA  
 CC encoding human IgG1 constant region (see AAV70079), and is deposited  
 CC as FERM BP-6074 (Glatmed). The invention provides methods for  
 CC producing humanised antibodies by culturing host cells. Humanised  
 CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
 CC of inducing apoptosis in abnormal cells expressing Fas, and of  
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
 CC antibodies are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to  
 CC treat such diseases, including autoimmune disease (e.g. systemic

CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
 CC autoimmune hemolytic anaemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura and  
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX  
 SQ Sequence 470 AA:  
 Query Match 78.7%; Score 566.5; DB 19; Length 470;  
 Best Local Similarity 78.6%; Pred. No. 2.9e-41;  
 Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
 QY 1 MGNKIIFFLYTATNGVHSQVLQVSGAEVKKPGSSVYVSKASGYPTTDAIQWRAP 60  
 DB 1 mgwscilfflvatalgvsqvlvsgaeavkpgasvskasgytltsymgmwvqap 60  
 OY 61 GGGLEWIGVINIYDNTVYNQKFKATPTVDKSTAYMELSLRSEDYAVYCARAA- 119  
 DB 61 ggrlewmgeidsdsytrnqkfkqkalitvdstastaymelslrsestdvyyccarrnd 120  
 QY 120 ---WYMDYMGQGLTVTVSS 135  
 DB 121 ysnwvfdvqwgqtlvtvss 140  
 RESULT 15  
 AAB14776  
 ID AAB14776 standard; Protein: 470 AA.  
 XX  
 AC AAB14776;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised; antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;  
 KW hepatitis; AIDS; graft rejection; heavy chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 OS  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 PI WPI: 2000-485645/43.  
 DR N-PSDB; AAA72159.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 PS Claim 21; Page 95-96; 139pp; Japanese.  
 CC The invention relates to compositions for the prevention or treatment  
 CC of diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs







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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:57:46 ; Search time 20.74 Seconds  
(without alignments)  
158,990 Million cell updates/sec

Title: US-09-249-011-6

Perfect score: 720  
Sequence: 1 MGNWCIFFLVTTATGVHSQ.....ARAAWYDWGQGLTVVSS 135

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCtus.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfilest1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573.5	79.7	140	4	US-08-579-378A-12
2	573.5	79.7	140	5	PCT-US93-11612-12
3	545	75.7	135	1	US-07-634-278-19
4	545	75.7	135	1	US-08-477-728-19
5	545	75.7	135	1	US-08-474-040-19
6	545	75.7	135	2	US-08-487-200-19
7	545	75.7	135	2	US-08-303-569B-31
8	545	75.7	135	4	US-08-484-537-19
9	531.5	73.8	163	5	PCT-US91-02842-5
10	530.5	73.7	140	3	US-08-836-561-63
11	530	73.6	467	2	PCT-US91-098A-45
12	529.5	73.5	136	5	PCT-US93-11611-11
13	529.5	73.5	138	3	US-08-513-968-44
14	529	73.5	139	2	US-08-656-586-8
15	527	73.2	135	1	US-08-137-117D-102
16	527	73.2	135	2	US-08-436-717-102
17	526	73.1	133	4	US-08-718-323A-8
18	525	72.9	139	1	US-08-253-877C-19
19	525	72.9	139	2	US-08-452-164A-19
20	525	72.9	139	3	US-08-603-024-18
21	521	72.4	135	1	US-08-137-117D-100
22	521	72.4	135	2	US-08-436-717-100
23	521	72.4	137	3	US-08-513-968-38
24	518.5	72.0	140	3	US-08-836-561-74
25	515.5	71.6	140	3	US-08-836-561-78
26	515	71.5	135	1	US-08-137-117D-112
27	515	71.5	135	2	US-08-436-717-112

28	511.5	71.0	136	4	US-08-525-539A-63	Sequence 63, Appl
29	508.5	70.6	143	1	US-08-236-520-7	Sequence 7, Appl
30	508.5	70.6	143	5	PCT-US95-05262-7	Sequence 7, Appl
31	507.5	70.5	140	3	US-08-836-561-83	Sequence 83, Appl
32	504.5	70.1	136	4	US-09-450-520A-8	Sequence 8, Appl
33	503.5	69.9	140	1	US-07-946-421-28	Sequence 28, Appl
34	501.5	69.7	123	1	US-08-482-882-53	Sequence 53, Appl
35	501.5	69.7	123	2	US-08-483-389-53	Sequence 53, Appl
36	501.5	69.7	123	2	US-08-487-113D-53	Sequence 53, Appl
37	501.5	69.7	123	2	US-08-473-503-53	Sequence 53, Appl
38	501.5	69.7	123	2	US-08-483-932-53	Sequence 53, Appl
39	501.5	69.7	123	3	US-08-720-420A-53	Sequence 53, Appl
40	501.5	69.7	123	3	US-08-714-017-53	Sequence 53, Appl
41	501.5	69.7	123	3	US-08-475-680-53	Sequence 53, Appl
42	500.5	69.5	142	2	US-08-476-176B-14	Sequence 14, Appl
43	500.5	69.5	142	3	US-08-127-721A-14	Sequence 14, Appl
44	500.5	69.5	142	3	US-08-485-246A-14	Sequence 14, Appl
45	499	69.3	128	4	US-09-199-149-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-08-579-378A-12  
Sequence 12, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: CO, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579, 378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160, 074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983, 946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschultz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-579-378A-12

Query Match	79.7%;	Score 573.5;	DB 4;	Length 140;
Best Local Similarity	78.6%;	Pred. No. 3.7e-50;		
Matches 110; Conservative	8;	Mismatches 17;	Indels 5;	Gaps 1;

Qy	1	MGAMNCIIIEFLVATATGAGSHQVQLVQSGAEYKKPSSSVKYSCKASGFTFTYALAIOWVQAP	60
Db	1	MGMSCIILFLVATATGAGSHQVQLVQSGAEYKKPSSSVKYSCKASGYFTFTSYVHHVWQAP	60
Qy	61	GGGSEMIIGVIVITYDDNNYNNQNKFKGATMYDKSTSTAYMELSLSRSEDTAYVYICAAAN	120
Db	61	GGGLEMIIGVITYDDNNYNNQNKFKGATMYDKSTSTAYMELSLSRSEDTAYVYICAREEY	120
Qy	121	-----YMDYMGQGTLYVSS	135
Db	121	GNIVRYTFDVMGQGTLYVSS	140

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: RESULT 2
: PCT-US93-11612-12
: Sequence 12. Application PC/TUS9311612
: GENERAL INFORMATION:
: APPLICANT: Co, Man Sung
: TITLE OF INVENTION: Humanized Antibodies Reactive with
: TITLE OF INVENTION: L-Selectin
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: One Market Plaza, Stewart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/11612
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/983,946
: FILING DATE: 01-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-22
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 140 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US93-11612-12

```

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Query Match      79.74: Score 573.5: DB.5: Length 140;
Best Local Similarity 78.68: Pred. No.3.7e-50;
Matches 110; Conservative 8; Mismatches 17; Indels 5; Gaps 1

QY 1 MGNMCIIFLLVTTATGVSHOVQVVGSGAEVKKRPGSSVKVSKASGDTFFDYAIQWVRQAP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGNMCIIFLLVATATGVSHOVQVVGSGAEVKKRPGSSVKVSKASGDTFFSYVMHWVRQAP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GCGLEMGIVINYYDNTNINQKFRKAKMTIVDKSTATMELSSLRSEETAYYYCRAAM 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 61 GGGLEMGICIIYPYNDGCTYNNKFKGRVITISDESTNIAINHELSLRBEDIAVYACAREEY 120  
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 QY 121 -----YMDYWGCGTLVTVSS 135  
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 Db 121 GNYVRYFDVWGQGLTVTVSS 140

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RESULT 3 |
US-07-634-278-19 |
: Sequence 19, Application US/07634278
: Patent No. 5530101
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/634,278
: FILING DATE: 19-DEC-1990
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002600
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEO, ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-07-634-278-19

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Query Match	75.7%	Score 545	DB 1	Length 135
Best Local Similarity	77.8%	Pred. No. 2.5e-47		
Matches 105	Conservative 7	Mismatches 23	Indels 0	Gaps 0
QY	1	MGNMNIIFELVATTAAGVSHOVQVLOSAGAEVKKRPGSSVKVSCASGTFPDYAIOWVROAP	60	
DB	1	MGMWMIFFLLSGTAGVSHOVQVLOSAGAEVKKRPGSSVKVSCASGTFPTSYRHHWVROAP	60	
QY	61	GAGLEWICIVINYYONTNVNOKFKGAKATPVKSTSTAYAMELSSLRSEDTAYAYCARAAW	120	
DB	61	GAGLEWICIVINPSTYETLENOKFKAKATITADESTNTATAMELSSLRSEDTAYAYCARGGG	120	

Qy	1	MGANCIIFELTATATGSHQVOLVOSAEVKKPSSSVKSCSKSGYFTDTALOWROAP	60
Db	1	MGMSEIFLELLSAGVASHQVOLVOSAEVKKPSSSVKSCSKSGYFTSTRYHHWRQAP	60
Qy	61	GQGLEMGVINYIYDNNINYNQKFKGKATMTYDKSTSTAVWELSLRSREDPAVYYCAAAW	120
Db	61	GQGLEMGVINYPSGVYEYNQKFKDKATTTADESTNAVWELSLRSREDPAVYYCAAGG	120



Db 121 VEDYWGQGLTVVSS 135

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RESULT 6
US-08-487-200-19
: Sequence 19, Application US/08487200
: Patent No. 5693762
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
: APPLICANT: SELICK, Harold E.
: TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,200
: FILING DATE: 7-JUN-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/634,278
: FILING DATE: 19-DEC-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/590,274
: FILING DATE: 28-SEP-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/310,252
: FILING DATE: 13-FEB-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/290,975
: FILING DATE: 28-DEC-1988
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-002610
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-487-200-19
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Query Match 75.7%; Score 545; DB 1; Length 135;  
Best Local Similarity 77.8%; Pred. No. 2.5e-47;  
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

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QY 1 MGNMCIFFLVTTATGVSHQVQVQSGAEVKKPGSSVSVKSCASGYFTDYAIDQWVRQAP 60
   ||| | |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGNMCIFFLVTTATGVSHQVQVQSGAEVKKPGSSVSVKSCASGYFTDYAIDQWVRQAP 60
QY 61 GGGLEMGIVINITYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAAW 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dk 61 GGGLEMGIVINIPSTGYEYNGKFKDKATITADESTNTAYMELSLRSRSDTAVVYCARGGG 120
QY 121 YMDYWGQGLTVVSS 135
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Db 121 VEDYWGQGLTVVSS 135

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RESULT 7
US-08-303-569B-31
: Sequence 31, Application US/08303569B
: Patent No. 5859205
: GENERAL INFORMATION:
: APPLICANT: Adair, John R.
: APPLICANT: Athwal, Diljeet S.
: APPLICANT: Emtage, John S.
: TITLE OF INVENTION: Humanised Antibodies
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205-15
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM/PC compatible
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/303,569B
: FILING DATE: 07-SEP-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Trujillo, Doreen Yanko
: REGISTRATION NUMBER: 35,719
: REFERENCE/DOCKET NUMBER: CARP-0032
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 135 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-303-569B-31
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Query Match 75.7%; Score 545; DB 2; Length 135;  
Best Local Similarity 77.8%; Pred. No. 2.5e-47;  
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

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QY 1 MGNMCIFFLVTTATGVSHQVQVQSGAEVKKPGSSVSVKSCASGYFTDYAIDQWVRQAP 60
   ||| | |||: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MGNMCIFFLVTTATGVSHQVQVQSGAEVKKPGSSVSVKSCASGYFTDYAIDQWVRQAP 60
QY 61 GGGLEMGIVINITYDNTNINOKFKGKATMTYDKSTSTAYMELSLRSRSDTAVVYCARAAW 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GGGLEMGIVINIPSTGYEYNGKFKDKATITADESTNTAYMELSLRSRSDTAVVYCARGGG 120
QY 121 YMDYWGQGLTVVSS 135
Db 121 VEDYWGQGLTVVSS 135

RESULT 8
US-08-484-537-19
: Sequence 19, Application US/08484537
: Patent No. 6180370
: GENERAL INFORMATION:
: APPLICANT: QUEEN, Cary L.
: APPLICANT: CO, Man Sung
: APPLICANT: SCHNEIDER, William P.
: APPLICANT: LANDOLFI, Nicholas F.
: APPLICANT: COELINGH, Kathleen L.
```

```

APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-537-19

Query Match          75.7%: Score 545; DB 4; Length 135;
Best Local Similarity 77.8%: Pred. No. 2.5e-47;
Matches 105; Conservative 7; Mismatches 23; Indels 0; Gaps 0;

QY      1  MGWNCIEFLVTTATGVASVOLVQSGAEVKKPGSSVYSCVCSAGSYTFETDVAIQWVRQAP 60
       | | | : | | | : | | | | | | | | | | | | | | | | | : | | | |
Db      1  MGSNIFLFLLSGLTGVASVOLVQSGAEVKKPGSSVYSCVCSAGSYTFTSYMMHVRQAP 60
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      61  GGGLEIGIVINIYDNTNYNQFKGKATMYTDKSTIAYAMELSSIRSEDTAVYYCARAAW 120
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  GGGLEIMICYINPSTGYETYNOKFKDKATITADESTNTAYMEELSRSEDTAVYYCARGGG 120
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      121 YMDYGOGTLVTSS 135
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 VFDYMGOGTLVTSS 135
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      9
PCT-US91-02942-5
Sequence 5, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:

```

[illegible]

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-836-561-63

Query Match 73.78; Score 530.5; DB 3; Length 140;  
Best Local Similarity 73.68; Pred. No. 7.2e-46;  
Matches 103; Conservative 11; Mismatches 21; Indels 5; Gaps 2;

QY 1 MGNACIEFLVTATGVHSGVQLVDSGAEVKKPGSSVSKASGYFTDYAIGWRAP 60  
DB 1 MEMWITFLISGTAGHSEVQLVDSGAEVKKPGASVSKASGYFTSYIHWRAP 60  
QY 61 GGGLEWIGVITNYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDYAVVYCARAA- 119  
DB 61 GGGLEWIGVITNYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDYAVVYCARAA- 119  
QY 120 -WY---MDYWGQGLVTVSS 135  
DB 121 RYVGLDGYWGQGLVTVSS 140

RESULT 11  
US-07-916-098A-45  
Sequence 45, Application US/07916098A  
Patent No. 5871732  
GENERAL INFORMATION:  
APPLICANT: BURKLY, LINDA C.  
APPLICANT: CHISHOLM, PATRICIA L.  
APPLICANT: THOMAS, DAVID W.  
APPLICANT: ROSA, MARGARET D.  
APPLICANT: ROSA, JOSEPH J.  
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN  
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.  
STREET: 10 SOUTH WACKER DRIVE  
CITY: CHICAGO  
STATE: ILLINOIS  
COUNTRY: U.S.A.  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/916,098A  
FILING DATE: July 24, 1992  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US91/08843  
FILING DATE: No. 5871732ember 27, 1991  
CLASSIFICATION: 424  
APPLICATION NUMBER: 07/618,542  
FILING DATE: No. 5871732ember 27, 1990  
ATTORNEY/AGENT INFORMATION:  
NAME: JOHN J. MC DONNELL  
REGISTRATION NUMBER: 26,949  
REFERENCE/DOCKET NUMBER: 92,310-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 715-1000  
TELEFAX: (312) 715-1234  
TELEX: 910/221-5317  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-916-098A-45

Query Match 73.68; Score 530; DB 2; Length 467;  
Best Local Similarity 72.58; Pred. No. 3.5e-45;  
Matches 103; Conservative 11; Mismatches 20; Indels 8; Gaps 2;

QY 1 MGNACIEFLVTATGVHSGVQLVDSGAEVKKPGSSVSKASGYFTDYAIGWRAP 60  
DB 1 MDWTVRVCCLAVAPGASHSQVQLDSGAEVKKPGASVSKASGYFTSYIHWRAP 60  
QY 61 GGGLEWIGVITNYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDYAVVYCAR-- 117  
DB 61 GGGLEWIGVITNYDNTNRYNOKFKGKATMTVDKSTSTAYMELSLRSEDYAVVYCAR-- 117  
QY 118 ----AAYMDYWGQGLVTVSS 135  
DB 121 NYATGAMFA-YWGQGLVTVSS 141

RESULT 12  
PCT-US93-11611-11  
Sequence 11, Application PC/TUS9311611  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
APPLICANT: Landolfi, Nicholas F.  
TITLE OF INVENTION: Humanized Antibodies Reactive with CD18  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourile and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11611  
FILING DATE: 30-NOV-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,949  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.



```

; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCRDUS93-11611-11

Query Match      73.5%; Score 529.5; DB 5; Length 136;
Best Local Similarity 75.7%; Pred. No. 8.8e-46;
Matches 103; Conservative 10; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGWNCIFLVTATGVHSQVQVLSGAEVKKFGSSVYKVSCKASGYTFDYAIQWRQAP 60
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Db 1 MGSMWIFLFLSGTAGVHSQVQVLSGAEVKKFGSSVYKVSCKASGYTFDYLMHWKQAP 60

QY 61 GGGLEWIGVINIYDNNYNQKFKATMTVDKSTAYAMELSLRSDPAVYYCAHAA- 119
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Db 61 GGGLEWIGNINPSTATDYDYNQNDKATLTADSTNATYELSLRSDPAVYYCANGGD 120

QY 120 WYMDYWGQGTLYTVSS 135
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Db 121 FLMDYWGQGTLYTVSS 136

RESULT 13
US-08-513-968-44
; Sequence 44, Application US/08513968
; Patent No. 6114143
; GENERAL INFORMATION:
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
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; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-513-968-44

Query Match      73.5%; Score 529.5; DB 3; Length 138;
Best Local Similarity 73.9%; Pred. No. 8.9e-46;
Matches 102; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

QY 1 MGWNCIFLVTATGVHSQVQVLSGAEVKKFGSSVYKVSCKASGYTFDYAIQWRQAP 60
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Db 1 MDWTRVRFCLLAAPGASHQVQVLSGAEVKKFGASVYKVSCKASGYTFDYPIEMKQNP 60

QY 61 GGGLEWIGVINIYDNNYNQKFKATMTVDKSTAYAMELSLRSDPAVYYCAHAA---R 117
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Db 61 GGGLEWIGNHPYSDNNYNEKFKAKLTVDISTNATYELSLRSDPAVYYCAIHYG 120

QY 118 AAWMDYWGQGTLYTVSS 135
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Db 121 SAYAMDYWGQGTLYTVSS 138

RESULT 14
US-08-556-586-8
; Sequence 8, Application US/08656586
; Patent No. 5834597
; GENERAL INFORMATION:
; APPLICANT: Tso, J. Yun
; APPLICANT: Anasetti, Claudio
; TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
; TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/656,586
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-007210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-656-586-8

Query Match      73.5%; Score 529; DB 2; Length 139;
Best Local Similarity 74.1%; Pred. No. 1e-45;
Matches 103; Conservative 10; Mismatches 22; Indels 4; Gaps 1;
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OY 1 MGWNCIFLVTATGVSQVQLVQSGAEVKKPKSSVKVSKASGYTFTDYAIQWVROAP 60  
 DB 1 MGWNCIFLVTATGVSQVQLVQSGAEVKKPKSSVKVSKASGYTFTDYAIQWVROAP 60  
 OY 61 GGGLEWIGVINIYDNTNNYKFKGKATMTVDKSTSTAYMELSLRSEDPAVYYCARAAW 120  
 DB 61 GGGLEWIGVINIYDNTNNYKFKGKATMTVDKSTSTAYMELSLRSEDPAVYYCARAAW 120  
 OY 121 YMDYWGOGTLVTYSS 135  
 DB 121 YMDYWGOGTLVTYSS 135

RESULT 15  
 US-08-137-117D-102  
 ; Sequence 102, Application US/08137117D  
 ; Patent No. 5795965

GENERAL INFORMATION:  
 APPLICANT: TSUCHIYA, Masayuki  
 APPLICANT: SATO, Koh  
 APPLICANT: BENDIG, Mary  
 APPLICANT: JONES, Steven  
 APPLICANT: SALDANHA, Jose  
 TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
 NUMBER OF SEQUENCES: 158  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Foley & Lardner  
 STREET: 3000 K Street, N.W., Suite 500  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentlin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/137,117D  
 FILING DATE: 20-DEC-1993  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/JP92/00544  
 FILING DATE: 24-APR-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 4-32084  
 FILING DATE: 19-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 3-95476  
 FILING DATE: 25-APR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: WEGNER, Harold C.  
 REGISTRATION NUMBER: 25,258  
 REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 102:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 135 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-137-117D-102

Query Match 73.2%; Score 527; DB 1; Length 135;  
 Best Local Similarity 75.6%; Pred. No 1.5e-45;  
 Matches 102; Conservative 8; Mismatches 25; Indels 0; Gaps 0;

OY 1 MGWNCIFLVTATGVSQVQLVQSGAEVKKPKSSVKVSKASGYTFTDYAIQWVROAP 60

DB 1 MDWTWRFCLLAIPAASQVQLVQSGAEVKKPKSSVKVSKASGYTFTSYIHVWROAP 60  
 OY 61 GGGLEWIGVINIYDNTNNYKFKGKATMTVDKSTSTAYMELSLRSEDPAVYYCARAAW 120  
 DB 61 GGGLEWIGVIDPFGGTSTNNYKFKGKATMTVDKSTSTAYMELSLRSEDPAVYYCARAGN 120  
 OY 121 YMDYWGOGTLVTYSS 135  
 DB 121 RFATYWGOGTLVTYSS 135

Search completed: August 26, 2002, 15:00:19  
 Job time: 153 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 15:37:07 ; Search time 1863.47 Seconds

(without alignments)  
4447.031 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 1 atggtacacagcagccaggt.....ggaccaagtcggaataaaa 396

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: GenEmbl:\*  
2: gb\_hcga:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_ph:\*  
7: gb\_pl:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: em\_da:\*  
15: em\_fun:\*  
16: em\_hum:\*  
17: em\_in:\*  
18: em\_inu:\*  
19: em\_om:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_un:\*  
28: em\_vl:\*  
29: em\_hcga:\*  
30: em\_hcga\_inv:\*  
31: em\_hcga\_inv:\*  
32: em\_hcga\_inv:\*  
33: em\_hcga\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Match Length DB ID Description

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3	336.2	84.9	406	10	MM062050	U62050 Mus musculus
4	333.6	84.2	419	10	MM097570	U97570 Mus musculus
5	332	83.8	940	6	A44968	A44968 Sequence 24
6	332	83.8	940	6	I64459	I64459 Sequence 24
7	301.4	76.1	401	10	MM1A21LEV	X65774 M.musculus
8	298.2	75.3	402	10	MUSICKALA	M68042 Mouse Ig re
9	296	74.7	336	10	AF163745	AF163745 Mus muscu
10	296	74.7	336	10	MDIGKVAR	Z22063 M.domesticu
11	296	74.7	339	10	AB028876	AB028876 Mus muscu
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13	295	74.5	339	10	MUSICKV130	L16819 Mus musculus
14	292.8	73.9	336	10	MDIGKVAI	Z22039 M.domesticu
15	292.8	73.9	336	10	MDIGKVAU	Z22070 M.domesticu
16	288.6	72.9	399	6	A47611	A47611 Sequence 3
17	288.6	72.9	399	6	A80111	A80111 Sequence 3
18	286.4	72.3	336	10	MM1222607	AJ222607 mouse DNA
19	286.4	72.3	337	10	S74056	S74056 Ig VKI-19G2
20	285.4	72.1	439	6	A62621	A62621 Sequence 40
21	285.4	72.1	460	6	A62617	A62617 Sequence 36
22	284.8	71.9	336	10	MM1KACLV	Z31353 M.musculus
23	284.8	71.9	336	10	MUSICKADU	M37022 Mouse Ig re
24	284.8	71.9	336	10	MUSICKADY	M37023 Mouse Ig re
25	284.8	71.9	339	10	MM060464	U60464 Mus musculus
26	284.4	71.8	336	10	MM055647	U55647 Mus musculus
27	284.2	71.8	336	10	MM055674	U55674 Mus musculus
28	283.2	71.5	336	10	MDIGKVAQ	Z22060 M.domesticu
29	283.2	71.5	342	6	AR135863	AR135863 Sequence
30	281.8	71.2	764	10	MMY15982	Y15982 Mus musculus
31	281.6	71.1	339	10	MM0344368	AJ344368 Mus muscu
32	281.6	71.1	600	10	AF349145	AF349145 Mus muscu
33	281.4	71.1	336	10	MM055673	U55673 Mus musculus
34	280.6	70.9	399	10	MUSFABA	M95574 M.musculus
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36	279.8	70.7	1443	6	AR063210	AR063210 Sequence
37	279	70.5	427	6	A94042	A94042 Sequence 23
38	279	70.5	427	6	AX011127	AX011127 Sequence
39	279	70.5	463	6	AR109948	AR109948 Sequence
40	279	70.5	8068	6	A94046	A94046 Sequence 27
41	279	70.5	8068	6	AX011131	AX011131 Sequence
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#### ALIGNMENTS

RESULT 1  
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LOCUS Mus musculus Igk chain (anti-Pseudomonas aeruginosa lipoprotein I  
DEFINITION Mus musculus Igk chain (anti-Pseudomonas aeruginosa lipoprotein I  
M28833.1 GI:576599  
ACCESSION M28833  
VERSION V-segment; anti-lipoprotein antibody; immunoglobulin kappa-chain;  
KEYWORDS immunoglobulin light chain.  
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) hybridoma CDNA  
to mRNA.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 462)  
AUTHORS Marget,M., Eckhardt,A., Ehret,W., von Specht,B.U., Duchene,M. and  
Domdey,H.  
TITLE Cloning and characterization of cDNAs coding for the heavy and  
light chains of a monoclonal antibody specific for Pseudomonas  
aeruginosa outer membrane protein I  
JOURNAL Gene 74 (2), 335-345 (1988)  
MEDLINE 89232725  
COMMENT On Nov 28, 1994 this sequence version replaced gi:342017.



JOURNAL J Immunol. 158 (2), 968-976 (1997)  
MEDLINE 97146071  
REFERENCE 2 (bases 1 to 406)  
AUTHORS Diaw, L., Magnac, C., Pritsch, O., Buckle, M., Alzari, P.M. and Dighiero, G.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUN-1996) Laboratoire d'Immunohematologie et d'Immunopathologie, Institut Pasteur, 28, rue du Dr. Roux, Paris 75724 Paris Cedex 15, France  
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source Location/Qualifiers  
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Best Local Similarity 92.7%; Pred. No. 4.1e-102;  
Matches 353; Conservative 0; Mismatches 28; Indels 0; Gaps 0;  
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Db 1 CAGGTTCTTATATTGCTGCTGCTATGGGATATGTRACCTGGGGACATTTGATGTCA 60  
QY 76 cagctccagatccctgctgtaagcttagagagagagagagagagagagagagagagag 135  
Db 61 CAGTCTCACTCCCTGGCTGTGTGTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120  
QY 136 agtccagatctgtctcaacagtagaacccagagagagagagagagagagagagagag 195  
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QY 196 ccagggcagcctctaaactgctgacttactggtgagcattgagagagagagagagag 255  
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QY 256 gatcgcttaagtgagtgagatctggagacagattcactctcaccatcagcagctctgac 315  
Db 241 GATCGCTTACAGGACAGGAGTGGATCTGGAGACAGATTTCACCTCACACATCAGCAGAGT 300  
QY 316 gctgaagagctggcagattatctactcagcagcattatattatcttcaacagttcgcag 375  
Db 301 GCTGAAGAGCTGGCAGCTTATTAATCTCAAGCAATTTAATATCTGTAACGTTCCGAGGG 360  
QY 376 ggagaccaaggtggaataaaa 396  
Db 361 GGGACCAAGCTGGAGATATAAA 381  
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MM097570 419 bp mRNA linear ROD 11-JUN-1997  
LOCUS Mus musculus immunoglobulin light chain variable region (Vgk) mRNA,  
DEFINITION partial cds.  
ACCESSION U97570 GI:2183076  
VERSION U97570.1  
KEYWORDS house mouse.  
SOURCE Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 419)  
AUTHORS Feijó, G.C.S., Sabbaga, J., Carneiro, C.R.M. and Brígido, M.M.  
TITLE Variable region structure and staphylococcal protein A binding specificity of a mouse anti-Iaminin receptor monoclonal IgM  
JOURNAL Immunology (1997) In press  
REFERENCE 2 (bases 1 to 419)  
AUTHORS Brígido, M.M.  
TITLE Direct Submission  
JOURNAL Submitted (15-APR-1997) Biologia Celular, Universidade de Brasília, Campus Universitario, Asa Norte, Brasília, DF 70910-900, Brazil  
FEATURES  
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/cell\_line="H12"  
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1..>419  
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BASE COUNT 105 a 101 c 115 g 98 t  
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Query Match 84.2%; Score 333.6; DB 10; Length 419;  
Best Local Similarity 90.2%; Pred. No. 3.1e-101;  
Matches 357; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
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QY 121 attagctgcaaatcaatcagatgctctcaacagtagaacccagagagagagagagag 180  
Db 141 ATGAGCTGCAAGTCCAGTCAAGTCTGCTCAMAAGTAGAACCCGAAAGAAATTAATCTGGCT 200  
QY 181 tgytaccagagaaacagagcagcctcctaactgtctgacttactgtggcaccactag 240  
Db 201 TGTATACAGAGAGAAACAGGAGCACTCCCAACTGCTGATCTACTGGCATCCACTAGG 260  
QY 241 gaactgtgggtccctgtactgcttcaagtgcagtgagatctggagacagattcactcacc 300  
Db 261 GAATCTGGGTCCTCGATCCCTTACAGCAGGAGTGGATCTGGAGACAGATTTCACACTCACC 320  
QY 301 atcagcagctgctgaggttgaagagcttgagcaggttatattacagcagcattataact 360  
Db 321 ATCAGCAGTGTGCAAGCTGAAGACCTGCAATTTATTAATTAATTAATTAATTAATCTT 380  
QY 361 tacacgttcgagacagaggaaggtggaataaaa 396  
Db 381 CGGACGTTGGGTGGAGGCCCCCAAGCTGGAAATCAAA 416  
RESULT 5  
A44968 940 bp DNA linear PAT 07-MAR-1997  
LOCUS A44968  
DEFINITION Sequence 24 from Patent WO9515382.  
ACCESSION A44968

VERSION A44968.1 GI:2299554  
 KEYWORDS unidentified.  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 940)  
 AUTHORS Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M., Wright, A.F., and Blakey, D.C.  
 TITLE BINDING STRUCTURES DIRECTED AGAINST THE CA55.1 ANTIGEN  
 JOURNAL Patent: WO 9515382-A 24 08-JUN-1995;  
 ZENECA LTD (GB)  
 COMMENT Other publication GB 2297751 950814  
 Other publication CA 2174972 950608  
 Other publication AU 9409266 950605  
 Other publication NZ 1113095 950619.  
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 Best Local Similarity 89.9%; Pred. No. 1.1e-100;  
 Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
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 Db 10 ATGATTACAGAGGCCAGGTTCTTATATTGCTGCTGATAGGATCTGGAACCTGAGG 69  
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 Db 70 GACATTGTGATGTCACAGTCTCCATCTCCCTGCTGCTGTGCAGCAGAGAGAAAGTCAAC 129  
 QY 121 attagctgcaaatccagctcagactcgtctcaacagttagaaccggagaactacttgct 180  
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 Db 130 ATGAGCTGCAAAATCCAGTCAAGAGTCTCTCAACAGTGAACCCGAAAGAACTACTTGCT 189  
 QY 181 tggtaaccagagaagaacaggagcagcctcctaactgtctgatacttacttgagatccactagg 240  
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 Db 190 TGGTACCAAGAGAGACAGGAGGAGTCTCTTAAGCTGCTGATCTATTGCGATCCACTAGG 249  
 QY 241 gaactctgggggtccctgactcgtctcagctgagctgagctgagacagattcactctcacc 300  
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 Db 250 ACATCTGGGGTCCCTGATCCCTTCATCCACAGCAGTGTGGACAGATTTCACCTCACC 309  
 QY 301 atcagcagctctgacagctgtaagaacgtgacgttatactactgcagcaacttataactct 360  
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 Db 310 ATCAGCAGTGTGACAGCTGGAAGACCTGGCAATTATTACTGCAAGCAATCTTATATCTT 369  
 QY 361 tacacgtctgacagagggacccaaggtggaataaaa 396  
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 Db 370 CGGACGTTCCGTTGGAGGACCAACCACTGGAATCAAA 405  
 RESULT 6  
 LOCUS 164459 940 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 24 from patent US 565357.  
 ACCESSION 164459  
 VERSION 164459.1 GI:2481353  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unidentified.  
 REFERENCE 1 (bases 1 to 940)  
 AUTHORS Rose, M.S., Boot, C., Copley, C.G., Paterson, D.S., Hall, S.M., Wright, A.F., and Blakey, D.C.  
 TITLE Hall, S.M., Wright, A.F., Paterson, D.S., and Blakey, D.C.  
 JOURNAL Antibodies recognizing tumor associated antigen CA 55.1  
 Patent: US 565357-A 24 09-SEP-1997;  
 FEATURES  
 source 1..940  
 Location/Qualifiers

BASE COUNT 241 a 266 c 213 g 220 t  
 ORIGIN  
 Query Match 83.8%; Score 332; DB 6; Length 940;  
 Best Local Similarity 89.9%; Pred. No. 1.1e-100;  
 Matches 356; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
 QY 1 atgattcacagagccagggttcctatatatgtcgtctgatatggtatctgacactgtg 60  
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 QY 241 gaactctgggggtccctgactcgtctcagctgagctgagctgagacagattcactctcacc 300  
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 QY 361 tacacgtctgacagagggacccaaggtggaataaaa 396  
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 Db 370 CGGACGTTCCGTTGGAGGACCAACCACTGGAATCAAA 405  
 RESULT 7  
 LOCUS MMLA21LEV 401 bp DNA linear ROD 15-JUN-1993  
 DEFINITION M.musculus DNA for Ige antibody light chain (VJ).  
 ACCESSION X65774  
 VERSION X65774.1 GI:312076  
 KEYWORDS Ige antibody; J-segment; light chain; V-region.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Kofler, H., Schneeg, I., Geley, S., Helmlberg, A., Varga, J.M. and Kofler, R.  
 TITLE Mechanism of allergic cross-reactions--III. cDNA cloning and variable-region sequence analysis of two Ige antibodies specific for trinitrophenyl  
 JOURNAL Mol. Immunol. 29 (2), 161-166 (1992)  
 MEDLINE 92178225  
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 source Location/Qualifiers  
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 /protein\_id="CAA4658.1"  
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Query Match 76.1%; Score 301.4; DB 10; Length 401;  
Best Local Similarity 86.5%; Pred. No. 2.3e-90;  
Matches 345; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

BASE COUNT 100 a 91 c 105 g 105 t  
ORIGIN

QY 1 atgattcaagagccaggtctctatatctgtctgtatgtggtatctgtgacctgtggg 60  
Db 3 ATGATTCAAGAGCCAGGCTTCTTATGTACTGCTGCTATGCGATCTGACCTGTGGG 62

QY 61 gacattgtctgacacagcttccagattccctgtgttaagcttagagagagggccact 120  
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QY 121 attagctgcaaatccagtcagagtcgtcaacagtagaacccgaggaactatttgct 180  
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Db 183 TGGTACACAGGGAACACAGGAGGTCTCTAACTGCTGATTTCTGGGATCCACTAGG 242

QY 241 gaattgtgggtccctgtatcgtcagtgagtgagtcgtggagacattcaactcacc 300  
Db 243 GAATCTGGGCTCCCTGATTCCTTCACAGGAGTGGATCTGGACAGATTTCACTCTCACC 302

QY 301 atcagcagctctgagagctggaagcgtgagttattactacagcaactctata---at 357  
Db 303 ATACAGCATGTGAAGGCTGAAGACCTGGCAGTTTATTTACTGTGCACTTATATAGCTCT 362

QY 358 ctctacacgtctcgacagagggagacaaagtgaataaaa 396  
Db 363 CCGTACACGTTGCGAGGGGGGACCAAGCTGGAATAAAA 401

RESULT 8  
LOCUS MUSIGKALA 402 bp mRNA linear ROD 14-JUL-1993  
DEFINITION Mouse Ig rearranged K-chain mRNA V-region, 5' end.  
ACCESSION M98042  
VERSION M98042.1 GI:196749  
KEYWORDS V-region; hepatitis; immunoglobulin light chain; processed gene.  
SOURCE Mus musculus (strain BALB/c, sub-species domesticus) spleen cDNA to mRNA.

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 402)  
AUTHORS Hong, H.-J., Kim, A.-K., Ryu, C.-J., Park, S.-S., Chung, H.-K., Kwon, K.-S.,  
Kim, K.-I., Kim, J., and Han, M.  
Cloning and characterization of cDNA's coding for heavy and light  
chains of a monoclonal antibody specific for pre-S2 antigen of  
hepatitis B virus  
JOURNAL Gene 121, 331-335 (1992)  
MEDLINE 93077049  
FEATURES  
source Location/Qualifiers  
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/organism="Mus musculus"  
/strain="BALB/c"  
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/tissue\_type="hybridoma"  
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/partial  
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virus"

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CDS

Query Match 75.3%; Score 298.2; DB 10; Length 402;  
Best Local Similarity 86.0%; Pred. No. 2.7e-89;  
Matches 343; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

BASE COUNT 102 a 93 c 100 g 107 t  
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61..402

QY 1 atgattcaagagccaggtctctatatctgtctgtatgtggtatctgtgacctgtggg 60  
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QY 61 gacattgtctgacacagcttccagattccctgtgtgttaagcttagagagagggccact 120  
Db 63 GACATTGTGATGTACAGTCTCCATTCCTCCTACCTGTGTCACTGGAGAGAGGTTACT 120

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Db 123 ATGAGCTGCAAGTCCAGTCAAGGCTTTTATATATAGTACATCAAAAGAACTACTTGGCC 180

QY 181 tggtaacagagaagaacacagagccctcctaactgtctatctactgtgcaaccactag 240  
Db 183 TGGTACACAGGGAACACAGGAGGTCTCTAACTGCTGATTTCTGGGATCCACTAGG 240

QY 241 gaattgtgggtccctgtatcgtcagtgagtgagtcgtggagacattcaactcacc 300  
Db 243 GAATCTGGGCTCCCTGATTCCTTCACAGGAGTGGATCTGGACAGATTTCACTCTCACC 300

QY 301 atcagcagctctgagagctggaagcgtgagttattactacagcaactctata---at 357  
Db 303 ATACAGCATGTGAAGGCTGAAGACCTGGCAGTTTATTTACTGTGCACTTATATAGCTAT 360

QY 358 ctctacacgtctcgacagagggagacaaagtgaataaaa 396  
Db 361 CCGTCAAGTTCGAGGGGGGACCTTACCTGGAATAAAA 399

RESULT 9  
LOCUS AF163745 336 bp mRNA linear ROD 20-JUL-2001  
DEFINITION Mus musculus mab 27.4.1 immunoglobulin light chain variable region  
ACCESSION AF163745  
VERSION AF163745.1 GI:5690296  
KEYWORDS house mouse.  
SOURCE Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 336)  
AUTHORS Mertens, N.M., Galvin, J.E., Adderson, E.E. and Cunningham, M.W.  
Molecular analysis of cross-reactive anti-mysin/anti-streptococcal  
mol. Immunol. 37 (15), 901-913 (2000)  
JOURNAL 21179651  
MEDLINE 11282394  
PUBMED 11282394  
REFERENCE 2 (bases 1 to 336)  
AUTHORS Mertens, N.M. and Cunningham, M.W.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1999) Microbiology and Immunology, Oklahoma  
University Health Sciences Center, 940 St. Young Blvd, Oklahoma  
City, OK 73190, USA  
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Location/Qualifiers

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BASE COUNT      91 a      83 c      86 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 10; Length 336;
Best Local Similarity 92.6%; Pred. No. 1.5e-88;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagcttccagattccctggctgtaagctagagagagccact 120
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QY 121 attagctgcaatccacagctcagagctctcacaagtagaacccgagagaacttgct 180
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DB 61 ATGAGCTGCAAATTCAGATCTGCTCAACAGTAGAACCAGAAAGAACTACTTGCT 120

QY 181 tggtagcagagaagaacagagcagctcctcaactctgactctacttgagatccactag 240
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QY 301 atcagcagctcgcagctgtagaagctgtagcttattactcgcagcgaacttataactct 360
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DB 241 ATCAGCAGCTGCGAGGCTGAAGACCTGCGAGTTATTACGCAAGCAATCTTAAATCTG 300

QY 361 tacacgttcgacagagggaccaaagtggaataaaa 396
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DB 301 TACACGTTGCGAGGGGAGGACCAAGCTGGAATAAAA 336

RESULT 10
MDICKVAR      336 bp      mRNA      linear      ROD 05-NOV-1994
DEFINITION    M.domesticus Igk variable region.
ACCESSION     Z22063
VERSION       Z22063.1 GI:297629
KEYWORDS      anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.
SOURCE        western European house mouse.
ORGANISM      Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.
1 (bases 1 to 336)
Both Igk and IgG anti-DNA antibodies are the products of clonally
selective B cell stimulation in (NZB x NZW)F1 mice
J. Exp. Med. 176 (3), 761-779 (1992)
92381444
2 (bases 1 to 336)
Marion,T.N.
Direct Submission
Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
Immunology, University of Tennessee, Memphis, 858 Madison Avenue,
Memphis, TN, 38163, USA
Location/Qualifiers
1. .336
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FGSGTKLEIK"

BASE COUNT      91 a      83 c      86 g      76 t
ORIGIN

Query Match      74.7%; Score 296; DB 10; Length 336;
Best Local Similarity 92.6%; Pred. No. 1.5e-88;
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagcttccagattccctggctgtaagctagagagagccact 120
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DB 61 ATGAGCTGCAAATTCAGATCTGCTCAACAGTAGAACCAGAAAGAACTACTTGCT 120

QY 181 tggtagcagagaagaacagagcagctcctcaactctgactctacttgagatccactag 240
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QY 361 tacacgttcgacagagggaccaaagtggaataaaa 396
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DB 301 TACACGTTGCGAGGGGAGGACCAAGCTGGAATAAAA 336

RESULT 11
AB028876      339 bp      mRNA      linear      ROD 07-DEC-1999
LOCUS         AB028876
DEFINITION    Mus musculus mRNA for 5.2 Igk light chain (variable region),
partial cds.
ACCESSION     AB028876
VERSION       AB028876.1 GI:5103290
KEYWORDS      5.2 Igk light chain variable region.
SOURCE        Mus musculus cell_line:hybridoma 5.2 cDNA to mRNA.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Yoshida,S., Matsuka,H., Luo,E., Iwai,K., Arai,M., Sinden,R.E. and
Ishii,A.
A single-chain antibody fragment specific for the Plasmodium
berghiei ookinete protein Pb21 confers transmission blockade in the
mosquito midgut
```

JOURNAL f  
MEDLINE 20058748  
REFERENCE 2 (bases 1 to 339)  
AUTHORS Yoshida,S.  
TITLE Direct Submision  
JOURNML Submitted (11-JUN-1999) Shigeto Yoshida, Jichi Medical School,  
Department of Medical Zoology, Yakushiji 3311-1,  
Minamikawachimachi, Tochigi 329-0498, Japan  
(E-mail:shigeto@jichi.ac.jp, Tel:81-285-58-7339,  
Fax:81-285-44-6489)  
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source Location/Qualifiers  
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BASE COUNT 92 a 84 c 87 g 76 t  
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Query Match 74.7%; Score 296; DB 10; Length 339;  
Best Local Similarity 92.6%; Pred. No.1.5e-88;  
Matches 311; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 61 gacattgtgcgcagacacatctccagattccctggtcgttaagttggaagagggccact 120  
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QY 361 taacacgttcgcagcagggagcaaggtggaataaaa 396  
Db 301 TACACGTTTGGAGGGGGGACCAAGCTGGAATAAAAA 336  
RESULT 12  
LOCUS S81289 408 bp mRNA linear ROD 23-MAY-1996  
DEFINITION Igm kappa chain variable region (CDR1 to CDR3 region) [rats, LEW,  
S81289  
ACCESSION S81289  
VERSION S81289.1 GI:1326409  
KEYWORDS  
SOURCE Rattus sp. LEW HAR-1 hybridoma cells.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.  
1 (bases 1 to 408)  
Borie,D.C., Cramer,D.V., Shirwan,H., Wu,G.D., Rodriguez,O.,  
AUTHORS Charman,F.A. and Makowka,L.  
TITLE Genetic control of the humoral immune response to xenografts. II.  
Monoclonal antibodies that cause rejection of heart xenografts are  
JOURNAL encoded by germ-line immunoglobulin genes  
MEDLINE Transplantation 60 (12), 1504-1510 (1995)  
REMARK 96125839  
Genbank staff at the National Library of Medicine created this  
entry [NCBI g1bbsq 176405] from the original journal article.  
This sequence comes from Fig. 4.  
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source Location/Qualifiers  
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BASE COUNT 106 a 100 c 108 g 94 t  
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Best Local Similarity 84.1%; Pred. No.2.8e-88;  
Matches 333; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
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Db 7 ATGATTCACAGACAGACAGGTCCTCATGTCCTGCTGCTGATCTGATCTGTGGG 66  
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Db 67 GACATTGTATGATGCCACCACTCCATCTCCACAGCTGTGTCAAGAGGAGAGGTCACT 126  
QY 121 attagctgcaaatccagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 180  
Db 127 ATGAGCTGCAAGTCCAGTCAGATCTTTTATACAAAGAAACAAAGAACTACTGGCC 186  
QY 181 tggtaaccagcagaaccagggcagcctcctaaactgctgatactcagtcagtcagtcagtcagtc 240  
Db 187 TGGTACACAGACAGAAACAGGCGAGTCTCTAAAGCTGATCTACTGCGGCGATCCACTAGG 246  
QY 241 gaattgggggtccctgattcgtctcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
Db 247 GAATCTGGGGTCCCTGATCGCTTTCATAGGCACTGAGTCTGGGACAGAAATTTCACCTCCACC 306  
QY 301 atcagcagctcgcagcgcgaagacgtgagcttattactgacgcaatctataactt 360  
Db 307 ATCAGCAGCTGTCAGGCGTGAACACTGCGCTGTTTATTACTGCGACGAGTACTTAACCTTG 366  
QY 361 taacacgttcgcagcagggagcaaggtggaataaaa 396  
Db 367 TACACGTTTGGAGCTTGGACCAAGCTGGAAGTAAA 402  
RESULT 13  
LOCUS MUSIGKV130 339 bp mRNA linear ROD 29-OCT-1994  
DEFINITION Mus musculus Ig rearrange kappa-chain gene V19-J1 region.  
ACCESSION L16619

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VERSION      L16819.1 GI:293622
KEYWORDS     V-region: complementarity determining region; immunoglobulin light
SOURCE       chain: kappa-immunoglobulin; processed gene.
ORGANISM     Mus musculus (strain NZB/W F1) mRNA.
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        Lustgarten,D.L., Kavalier,J., Gerhard,W. and Schaff,M.D.
JOURNAL      The response to a foreign antigen in the autoimmune NZB/W F1 murine
FEATURES     strain
SOURCE       Location/Qualifiers
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              /strain="NZB/W F1"
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              /standard_name="V19"
              1..339
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              70..102
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              148..168
              /gene="Igk-V19"
              /standard_name="CDR2"
              265..291
              /gene="Igk-V19"
              /standard_name="CDR3"
              286..324
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BASE COUNT
ORIGIN
Query Match      74.5%; Score 295; DB 10; Length 339;
Best Local Similarity 92.3%; Pred. No.3.2e-88;
Matches 310; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagctccagattccctgctgtaagcttagagagaaggccact 120
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DB 1 GACATTGTGATGTCAACAGCTCCATCCCTCCGCTGCTGTGTCAGACAGAGAGGTCAC 60

QY 121 attagctgcaaatccagctcagctgctgtctcaacagtagaaccggagagaactctgct 180
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DB 61 ATGAGCTGCAAAATCCAGTCCAGTCTGCTCAACAGTAGAACCCGAAGAACTACTTGCGCT 120

QY 181 tggtaaccagagaacccagagcgagctctcctaactctgatactctactgagcattccactagg 240
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QY 241 gaacttgagggtccctgatactgcttcagctgagctgagctcctggagacagattcactctcacc 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
DB 181 GAATCTGGGGTCCCTGATGCTTTCACAGGACAGTGTGGAGACAGATTTCACCTTCACC 240

QY 301 atcaacagctcagcagcagctgaagaagctgagcttattactatgcagcaactctataactct 360
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DB 241 ATTCACACAGTGTCTCAGAGCTGAAGACCTGAGATTATTTACTGCAAGCAATCTTATAATCT 300

QY 361 tacacgcttcgagcagggagcacaagtggaataaaa 396
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DB 301 TACACGCTTCGGAGGGGNGACCAAGCTGGAATRAAA 336

RESULT  J4
LOCUS    MDIGGVAI
DEFINITION M.domesticus Igg variable region.

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ACCESSION    222039
VERSION      222039.1 GI:297576
KEYWORDS     anti-DNA antibody; Igg gene; Igg variable region; immunoglobulin.
SOURCE       western European house mouse.
ORGANISM     Mus musculus domesticus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE        TILMAN,D.M., JON,N.T., HILL,R.J. and MARION,T.N.
JOURNAL      Both Igm and Igg anti-DNA antibodies are the products of clonally
FEATURES     selective B cell stimulation in (NZB x NZM)F1 mice
SOURCE       J. Exp. Med. 176 (3), 761-779 (1992)
MEDLINE     92381444
REFERENCE    2 (bases 1 to 336)
AUTHORS      Marion,T.N.
TITLE        Direct Submission
JOURNAL      Submitted (23-MAR-1993) Tony N. Marion, Microbiology and
              Immunology, University of Tennessee, Memphis, 858 Madison Avenue,
              Memphis, TN, 38163, USA
FEATURES     Location/Qualifiers
              1..336
              /organism="Mus musculus domesticus"
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              /db_xref="taxon:10092"
              /chromosome="6"
              /sex="Female"
              /cell_line="163.1"
              /cell_type="hybridoma"
              /tissue_type="spleen"
              /dev_stage="somatic variant"
              1..336
              /gene="Igk"
              <1..>336
              /gene="Igk"
              /function="Kappa light chain variable region for anti-DNA
              antibody; Vκ8 family"
              /note="163.1 is clonally related to the Igg hybridomas
              163.14, 163.37, 163.64, 163.77, 163.106, 163.124, 163.132,
              and 163.133 in the 163-cl clone"
              /codon_start=1
              /product="immunoglobulin variable region"
              /protein_id="CAA80013.1"
              /db_xref="GI:297577"
              /translation="DIVMSQPSLSAVSAGEKVTNCSKSSQSLNSRTRKNTLANYQ
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              FCGTKLEIK"
BASE COUNT   90 a 82 c 88 g 76 t
ORIGIN
Query Match      73.9%; Score 292.8; DB 10; Length 336;
Best Local Similarity 92.0%; Pred. No.1.8e-87;
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagctccagattccctgctgtaagcttagagagaaggccact 120
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DB 1 GACATTGTGATGTCAACAGCTCCATCCCTCCGCTGCTGTGTCACACAGAGAGAGGTCAC 60

QY 121 attagctgcaaatccagctcagctgctgtctcaacagtagaaccggagagaactctgct 180
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DB 61 ATGAGCTGCAAAATCCAGTCCAGTCTGCTCAACAGTAGAACCCGAAGAACTACTTGCGCT 120

QY 181 tggtaaccagagaacccagagcgagctctcctaactctgatactctactgagcattccactagg 240
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DB 121 TGGTACACAGCAAAACACAGGCAAGTCTCTTAACCTGCTACTACTGGGCAATCCACTAGG 180

QY 241 gaacttgagggtccctgatactgcttcagctgagctgagctcctggagacagattcactctcacc 300
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DB 241 GAATCTGGGGTCCCTGATGCTTTCACAGGACAGTGTGGAGACAGATTTCACCTTCACC 240

QY 301 atagcagctcagcagcagctgaagaagctgagcttattactatgcagcaactctataactct 360
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Db 241 ATCAGCAGTGTGCGAGCTGAAGACCTGGCAGTTATTACTGCAGCAATCTATATCTG 300

QY 361 tacacgttcgacagggagaccaggtggaataaa 396  
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Db 301 TACACGTTTCGGGGGGGGACCAAGCTGGAATATAAA 336

RESULT 15

MDICKVAV 336 bp mRNA linear ROD 05-NOV-1994

LOCUS M.domesticus Igk variable region. 222070

DEFINITION 222070.1 GI:297635

ACCESSION 222070

VERSION 222070.1

KEYWORDS anti-DNA antibody; Igk gene; Igk variable region; immunoglobulin.

SOURCE western European house mouse.

ORGANISM Mus musculus domesticus

REFERENCE 1 (bases 1 to 336)  
Tillman,D.M., Jou,N.T., Hill,R.J. and Marion,T.N.  
Both Igk and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice  
J. Exp. Med. 176 (3), 761-779 (1992)

MEDLINE 92381444

AUTHORS Marion,T.N.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of Tennessee, Memphis, 858 Madison Avenue, Memphis, TN, 38163, USA

FEATURES

source location/Qualifiers

1..336

/organism="Mus musculus domesticus"

/strain="(NZB x NZW)F1"

/isolate="mouse #165"

/db\_xref="taxon:10092"

/chromosome="6"

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/cell\_line="165.5"

/cell\_type="hybridoma"

/tissue\_type="spleen"

/dev\_stage="somatic variant"

1..336

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/gene="Igk"

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CDS

gene

BASE COUNT 91 a 83 c 86 g 76 t

ORIGIN

Query Match 73.9%; Score 292.8; DB 10; Length 336;  
Best Local Similarity 92.0%; Pred. No 1.8e-87;  
Matches 309; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 61 gacatgtcctgacacagctccagattccctgctgtaagcttagagagagagccact 120  
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Db 1 GACATGTGATGTCACAGCTCCATCCCTCGCTGTGCAGCAGAGAGAGAGTCACT 60

QY 121 attagctgaatccagtcagagctgctcaacagtagaaccgcgagagaactacttgct 180  
|||||  
Db 61 ATGAGCTGCAAAATCTGACAGAGCTGTCTCAACAGTAGAACCCGAAAGAACTACTTGGCT 120

QY 181 tgtaccacagaaacacaggtcagctcctaactgctgactcactgagcatcactagg 240  
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Db 121 TGGTACCAGCAGAAACAGGGCAGCTCTCTAACTGCTGATCTACTGGGCATCCACTAGG 180

QY 241 gaatctgggtcccttgatcgtctcagttgagtgagtgatctggagacagattcacttcacc 300  
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Db 181 GAATCTGGGTCCTCGATCGCTTCACAGGCAGTGATCTGGGACAGATTTCACCTCCACC 240

QY 301 atcagcagctcgcagagctggaagacgttgcaattattactgcagcagcatcttaactctt 360  
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Db 241 ATCAGCAGTGTGCGAGCTGAAGACCTGGCAGTTATTACTGCAGCAATCTATATCTG 300

QY 361 tacacgttcgacagggagaccaggtggaataaa 396  
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Db 301 TACACGTTTCGGGGGGGGACCAAGCTGGAATATAAA 336

Search completed: August 26, 2002, 15:37:10  
Job time: 2209 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 16:13:39 ; Search time 2170.14 Seconds

(without alignments)  
2462.880 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396  
Sequence: 1 atgattccacagcccaaggt.....ggaccaagtggaataaaa 396

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gD\_estcl:\*  
10: gD\_estl2:\*  
11: gD\_hic:\*  
12: gD\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	312	78.8	905	10	BF580037 602095235
2	288.6	72.9	864	10	BF111610 602895973
3	272.8	68.9	691	10	BF128999 601811318
4	269.4	68.0	850	10	BG9666217 602830177
5	267	67.4	575	10	BT249452 602995769
6	259.4	65.5	964	10	BG757678 602711268
7	258.6	65.3	300	10	BG148633 6025711268
8	256.6	64.8	798	10	BG426036 602492715
9	256	64.6	641	9	AM405821 602492715
10	253.4	64.0	643	9	AM390292 602492715
11	251	63.4	886	10	BF674779 602137932
12	249.2	62.9	633	10	BG542772 602571134
13	247.6	62.5	508	9	AM406572 602571134
14	247.6	62.5	819	10	BG686522 602637474
15	247.6	62.5	842	10	BG757770 602714482
16	247.6	62.5	887	10	BF663188 602144432
17	247	62.4	625	10	BT820438 603034746

18	247	62.4	876	10	BG397563 602438602
19	245.6	62.0	921	10	BG569993 602590249
20	245.4	62.0	710	10	BG537677 602566021
21	244	61.6	388	9	AM951579 EST363649
22	242.6	61.3	757	10	BG484518 602505173
23	242.6	61.3	767	10	BG541967 602569470
24	242.6	61.3	1057	10	BG399525 602568157
25	242.6	61.2	769	10	BG334966 602554155
26	242.2	61.2	761	10	BG336372 602564763
27	241.4	61.0	935	10	BG398034 602439564
28	241.2	60.9	698	10	BT600019 603044477
29	240.6	60.8	573	10	BT128829 601811013
30	240	60.6	745	10	BG484741 602505627
31	235.8	59.5	541	10	BG547312 602574731
32	234.4	59.2	869	10	BG429604 602501285
33	234.2	59.1	559	10	BG548150 602575305
34	233.6	59.0	878	10	BT837524 603087066
35	231.6	58.5	957	10	BG756233 602713544
36	231.4	58.4	862	10	BG485664 602505963
37	231.4	58.4	887	10	BT128587 601810838
38	229.6	58.0	401	9	AV685285 601810838
39	229.2	57.9	790	10	BG548131 602575878
40	228.4	57.7	533	9	AM802126 602575878
41	228.4	57.7	558	10	BF964753 602267977
42	227.2	57.4	503	10	BF830413 602267977
43	226.6	57.1	550	9	AM404610 602267977
44	226.2	57.1	403	9	AV734428 602267977
45	225.4	56.9	716	10	BG570035 602591008

#### ALIGNMENTS

RESULT 1  
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LOCUS 602095235F1 NCT\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4209417 5'  
DEFINITION mRNA sequence.  
ACCESSION BF580037  
VERSION BF580037.1 GI:11653749  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgc.ncl.nih.gov/  
1 (bases 1 to 905)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9775 row: f column: 10  
High quality sequence stop: 757.  
Location/Qualifiers  
1. 905  
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/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: colon; Vector: PCW-SPORE6; Site:1; Ncti; Site:2; Sali; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCT\_CGAP Library."  
BASE COUNT 248 a 236 c 217 g 204 t

## ORIGIN

Query Match 78.8%; Score 312; DB 10; Length 905;

Best Local Similarity 91.7%; Pred. No. 2e-85; Matches 363; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

QY 1 atgagtcacagagccaggtctctatattgctctgtctataggtatctgacacctgtg 60  
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QY 61 gacattgtctgacacagctctcagattccctgtgctgtaagcttaagagagagccact 120  
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Db 255 GAATCTGGGGTCCCTGATGCTTACAGAGCAGTGTGAGATCTGGACAGATTTCACCTCACC 314  
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Db 315 ATCAGAGTGTGAGGCTGAGAGCTGGCGAGTTATTACTGCAAGCAATCTTAAATCTT 374  
QY 361 tacacgtctcgacagagggacacagtcagtcagtcagtcagtcagtcagtcagtcagtc 396  
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Db 375 TTCACGTTGGCTCGGGGACAAAGTTGGAATATAA 410

## RESULT 2

LOCUS B111610 864 bp mRNA linear EST 26-JUN-2001  
DEFINITION 602895973F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:5025715 5',  
RNA sequence.

ACCESSION B111610  
VERSION B111610.1 GI:14562511  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 864)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapb-remail.nih.gov  
Tissue Procurement: Lotmar Hennighausen Ph.D., Robin Humphreys  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM1073 row: b column: 20  
High quality sequence stop: 644.  
Location/Qualifiers  
1..864

## FEATURES

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/tissue\_type="tumor, gross tissue"  
/dev\_stage="7 months"  
/lab\_host="DH10B"

BASE COUNT 230 a 233 c 196 g 205 t

/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigators  
providing samples: Lotmar Hennighausen/Robin Humphreys,  
NIH"

Query Match 72.9%; Score 288.6; DB 10; Length 864;

Best Local Similarity 84.5%; Pred. No. 3.2e-78; Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

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Db 2 ATGAGTTTCACAGGCCACAGGTTCTTATA-TGCTCTGCTATAGGTATCTGTGCTGTGG 61  
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Db 62 GACATTGTATGTACAGAGTCTCCATCCCTCCGCTGTGTGTCAGATTGAGAGAGATTACT 121  
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Db 122 ATGAGCTGCAAGTCCAGTCAAGCCTTTTATATATAGCAATCAATAAGAACTACTTGGCC 181  
QY 181 tggctacagagagaacacagagcagctcctcaactgtctgtactgtggagatcactagg 240  
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Db 182 TGGTACACAGCAGAAACCAAGGCGAGTCTCTTAACCTGCTATCTAGTGGCATCCACTAG 241  
QY 241 gaactctgggggtccctgctgctcagtcagtcagtcagtcagtcagtcagtcagtcagtc 300  
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Db 242 GAATCTGGGGTCCCTGATGCTTACAGAGCAGTGTGAGATCTGGACAGATTTCACCTCACC 301  
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Db 302 ATCAGAGTGTGAGGCTGAGAGCTGGCGAGTTATTACTGTCAGCAATTTTAACTAT 361  
QY 358 cttaacagctctcgacagagggacacagtcagtcagtcagtcagtcagtcagtcagtcagtc 396  
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Db 362 CCGTGACGTTCCGTGGAGGACCAAGCTGGAATATCAA 400

## RESULT 3

LOCUS BF128999 691 bp mRNA linear EST 24-OCT-2000  
DEFINITION 601811318F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4054205 5',  
RNA sequence.

ACCESSION BF128999  
VERSION BF128999.1 GI:10968039  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 691)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapb-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM894 row: c column: 06  
High quality sequence stop: 682.  
Location/Qualifiers  
1..691

## FEATURES

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"





CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1M11374 row: b column: 24  
 High quality sequence stop: 575.

## FEATURES

source

1..575  
 /organism="Mus musculus"  
 /strain="C57/B6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5151287"  
 /clone\_1lb="NCI CGAP Mam5"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="7 months"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Robin Humphreys,  
 NIH"

BASE COUNT 149 a 137 c 139 g 150 t  
 ORIGIN

## Query Match

Best Local Similarity 82.7%; Pred. No. 1.3e-71;  
 Matches 330; Conservative 0; Mismatches 65; Indels 4; Gaps 2;

OY 1 atggaattcacaagccaggtcttataatgtctgtctatggtatggtatcgtgacctgtgg 60  
 DB 9 atggaattcacaagccaggtcttataatgtctgtctatggtatggtatcgtgacctgtgg 68  
 OY 61 gacattgtctcaacagctcagatcctcgtgctgtaagcttagaagaagggccact 120  
 DB 69 gacattgtctcaacagctcagatcctcgtgctgtaagcttagaagaagggcttagc 128  
 OY 121 attagctgcaaaatccagtagagctctgctcaacagtagaaccgagagaactactggtc 180  
 DB 129 atgagctgcacagccagctcagatcctcgtgctgtaagcttagaagaagggccact 188  
 OY 181 tggtaaccagcagaagaacagagcagctcctctaaactgtctatctactggtgcatcactagg 240  
 DB 189 tggtaaccagcagaagaacagagcagctcctctaaactgtctatctactggtgcatcactagg 247  
 OY 241 gaatctggagctccctgattcagctcagtagagtagctggagacagatttctcacc 300  
 DB 248 gaatctggagctccctgattcagctcagtagagtagctggagacagatttctcacc 307  
 OY 301 atcagcagctctgcaagctggaagcgtgagcagttatctactgcaagcaatctata--at 357  
 DB 308 atcagcagctctgcaagcgtggaagcgtgagcagttatctactgcaagcaatctata--at 367  
 OY 358 ctttaacagcttgcgacagagggacaaagtgtggaataaaa 396  
 DB 368 cggctcagcttgcgacagagggacaaagtgtggaataaaa 406

## RESULT 6

LOCUS BG757678 964 bp mRNA linear EST 15-MAY-2001  
 DEFINITION 602711268P1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4851521 5',  
 mRNA sequence.  
 ACCESSION BG757678  
 VERSION BG757678.1 GI:14068331

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 964)  
 NIH-MGC <http://imgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgephs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CMI694 row: h column: 18  
 High quality sequence stop: 784.

## FEATURES

source

1..964  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4851521"  
 /clone\_1lb="NIH\_MGC\_48"  
 /tissue\_type="Primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI;  
 Site\_2: EcoRI; CDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library."

BASE COUNT 236 a 280 c 238 g 210 t  
 ORIGIN

## Query Match

Best Local Similarity 80.1%; Pred. No. 3.5e-69;  
 Matches 318; Conservative 0; Mismatches 76; Indels 3; Gaps 1;

OY 3 ggaattcacaagccaggtcttataatgtctgtctatggtatggtatcgtgacctgtgg 62  
 DB 1 ggaattcacaagccaggtcttataatgtctgtctatggtatggtatcgtgacctgtgg 60  
 OY 63 catctgtgcagacagctcctcagatccctcgtgctgtaagcttagaagaagggccact 122  
 DB 61 catctgtgcagacagctcctcagatccctcgtgctgtaagcttagaagaagggccact 120  
 OY 123 taagtcaaatccagtagagctctgctcaacagtagaaccgagagaactactggtc 182  
 DB 121 caactgcmaagctccagcagagctgtttatracactccacaaatracactactgcttg 180  
 OY 183 gtaccagcagaacccagggcagctcctctaaactgtctgattctactggtgcatcactagg 242  
 DB 181 gtaccagcagaacccagggcagctcctctaaactgtctgattctactggtgcatcactagg 240  
 OY 243 atctgggttccctgacatcgtctcagtagtgtagatctggagacagatttctcaccat 302  
 DB 241 atctgggttccctgacatcgtctcagtagtgtagatctggagacagatttctcaccat 300  
 OY 303 cagcagctctgcaagctggaagcgtgagcagttatctactgcaagcaatctata--taatc 359  
 DB 301 cagcagctctgcaagcgtggaagcgtgagcagttatctactgcaagcaatctata--taatc 360  
 OY 360 ttacacgttgcgacagagggacaaagtgtggaataaaa 396  
 DB 361 aagacagcttgcgacagagggacaaagtgtggaataaaa 397

## RESULT 7

LOCUS BG148633 300 bp mRNA linear EST 01-FEB-2001  
 DEFINITION u085b09.v1 Soares mouse\_NMGb cell mus musculus CDNA clone  
 IMAGE:3383368 5' similar to SW:KVC\_HUMAN P06314 IG KAPPA CHAIN  
 V-IV REGION J17 PRECURSOR. ; mRNA sequence.

[illegible]

ORGANISM	Human sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 798)
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: L10CM1345 row: n column: 03 High quality sequence stop: 542. Location/Qualifiers 1..798
FEATURES	<p>source</p> <p>1..798</p> <p>organism="Homo sapiens"</p> <p>db_xref="taxon:9606"</p> <p>clone="IMAGE:460658"</p> <p>clone_lib="NIH-MGC-75"</p> <p>/lab_host="IDH10B (T1 phage-resistant)"</p> <p>/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site.1: SfiI (ggcgccctggccc); Site.2: SfiI (ggccttatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCAGAGCCGAGGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."</p>
BASE COUNT	192 a 213 c 212 g 181 t
ORIGIN	
Query Match	64.8%; Score 256.6; DB 10; Length 798;
Best Local Similarity	79.4%; Pred. No. 2.4e-68;
Matches 317; Conservative	0; Mismatches 79; Indels 3; Gaps 1;
QY	1 atgattatcacagagcccaagttcttataatgtctgtcgtataggatcttgacacctgtgg 60
DB	31 ATGATGTCGACAGACCAGTCTTCATTTCTGTTGCTGTGATCTGATCTGATGCTGCTACGGG 90
QY	61 gacatttgctgcagacacgattctccagatccctgtgctgtgaagcttgagagagagggccact 120
DB	91 GACATCTGTGATGATGCCACCACTCTCCAAAGTCCCTCGGTGTCTCTGGGGAGAGGGCCACCC 150
QY	121 attagctgaataatccagtcagagctgtgtcttcaacagtagaaccccgagagaacactctggct 180
DB	151 ATCAACTGCAAGTCCAGCCAGAGCTTTTGTTCACACTCCACAAATTAAGAACTACTTAGTT 210
QY	181 tggtaacagagaaacacagggcagccctccaaactgtgattctactgtgagcatccactag 240
DB	211 TGGTACCGACGACAAACCGAGACAGCCCTCTAAACGTCAATTTCTCGGGGCACTACCCGG 270
QY	241 gaattgggtgtcccttgatcgcgttttagtgtagtgagttgtagagagatttaactctaac 300
DB	271 GAATCCGGGGTCCCTGCACGATTCAGTGTGGCAGCGGGGTGTGGACAGATTTCCTCTCACCC 330
QY	301 atcagcaatctgcagagcgtcgaagacgttgacagtttactctgacagcaatcttata---at 357
DB	331 ATCAGCACTGTGACAGGGCTGAAGATGTGGCAGATTATTTACTGGCACACAMTGTATGTGCT 390
QY	358 cttaacacgttcgcagagagagagcccaagttgaataataaa 396
DB	391 CCTCTCACTTTCGGCGGAGGAGCAAGGTTGAGATCAAA 429

AM405821 641 bp mRNA linear EST 16-FEB-2000  
 LOCUS UI-HF-BL0-abp-h-07-0-UI.r1 NIH\_MGC\_37 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3057636 5', mRNA sequence.  
 ACCESSION AM405821  
 VERSION AM405821.1 GI:6924878  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 641)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Eco RI site shown at the beginning of the sequence.  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 cDNA Library Arrayed by: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.lnl.gov/dbp/image/image.html](http://www.bio.lnl.gov/dbp/image/image.html)  
 Seq primer: M13 Forward.  
 Location/Qualifiers  
 1..641  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3057636"  
 /clone\_1lb="NIH\_MGC\_37"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LT1)"  
 /note="Vector: pT73-Pac; Site\_1: NotI; Site\_2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 159 a 178 c 163 g 141 t  
 ORIGIN

Query Match 64.6%; Score 256; DB 9; Length 641.  
 Best Local Similarity 81.0%; Pred. No. 3.3e-68;  
 Matches 311; Conservative 0; Mismatches 70; Indels 3; Gaps 1;

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QY 16 caggtcttataatgtctgtctgtatctggcacctgtggagacattgtgtgaca 75
    |||||  ||  ||  |||||  ||  |||||  ||  |||||  ||  |||||
Db  8 CAGGTCTTCATTTCTGTGCTGTGATCTGTGTCCTACAGGGAGCATGCTGATGAC 67

QY 76 caatctccagattccctgtctgaagcttagagagagagagacattatctgcaatcc 135
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  68 CACTCTCCACAGTCCCTGGCTGTCTCTGGGAGAGGGCCACACATCAACTGCACACTCC 127

QY 136 agcagagatctgtctcaacagtagaacccgagagaactactgtgtgtgacagagaaa 195
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  128 AGCCACAGATCTTTATACAGCTCCACACATTAAGAACTACTAGTTGTGTACACAGAAA 187

QY 196 ccaaggacagcctccctaaatcgtcatctactgtggcatcaccactaggaatctgggtccct 255
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  188 CCAGGGCAGCCTCTAAGCTGTCACTTACTGTGGCATCTACCGGGGAATCCGGGGTCCCT 247

QY 256 gatcgcctcaatgtgagtgatctggagacagattcaactcaacatcagcagtcgag 315
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  248 GACCGATTCAGTGGGCGGGGTGGGACAGATTTCACCTCCACACACAGCAGCTTCAG 307

QY 316 gctgaagacgtgagcttactgaacgaactctta--taactcttacagcttcgga 372
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  308 GCTGAGATGTGGCAGCTTTTACTGTGACGACATATTATAGTACTCTCGAGAGCTTCGGC 367
  
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QY 373 caggagaccaggtcgtgaatacaaa 396  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 368 CAGGGAGACCAAGGTGCAATCAAA 391

RESULT 10  
 LOCUS AM390292 643 bp mRNA linear EST 04-FEB-2000  
 DEFINITION CM2-ST0182-221099-023-f04 ST0182 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM390292  
 VERSION AM390292.1 GI:6894951  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 643)  
 AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t=CM2-ST0182-221099-023-f04&t3=199-10-22&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 7  
 High quality sequence stop: 641.  
 Location/Qualifiers  
 1..643  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1lb="ST0182"  
 /dev\_stage="Adult"  
 /note="Organ: Stomach; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (0.5. Letters Patent application  
 No. 196/716 - Ludwig Institute for Cancer Research)  
 Profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

BASE COUNT 162 a 173 c 162 g 146 t  
 ORIGIN

Query Match 64.0%; Score 253.4; DB 9; Length 643;  
 Best Local Similarity 78.9%; Pred. No. 2.1e-67;  
 Matches 315; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

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QY 1 atggaattcacagggccaggtctatataatctgtgtgcatatctggcacctgtggg 60
    |||||  ||  ||  |||||  ||  |||||  ||  |||||  ||  |||||
Db  9 ATGGTGTGAGAGACCAGGCTTCATTTCTGTGCTGTGATCTGTGGTGGCTACAGGG 68

QY 61 gaactgtctgacacagttccagattccctgtgctgaagcttagagagagggcact 120
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  69 GACATCTGTGATGACCAGTGTCCAGACTCCCTGGCTGTCTGTGGCGGAGAGGCCACC 128

QY 121 attagctgcaatccagtcaggtctgtctcaacagtagaacccgagagaactactgtgct 180
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  129 ATCAACTGCAAGTCCACCCAGAGATTATTATACAACTCCAAAATTAAGAACTACTTAGCT 188

QY 181 tggtaaccagagaacaacaggagcagcctccaaactgtgtactactgtgacatcaatagg 240
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db  189 TGGTACCAGAGAAACACGAGACAGCCTCTTAAGCTGCTCTTTACTGTGGCATCATCAGCGG 248

QY 241 gaatctgggtccctgtactgcttcagctgagtgagatctggagacagattcaactctaac 300
  
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Db	Accession	Source	Score	Length	Gap
Db	151 ATCAACTGCAAGTCCAGACGAGAGTCTTTATACACTCCACAAATAGACTACTTTCT	LOCUS BGS42772 633 bp mRNA linear EST 03-APR-2001	62.9%	249	2
Db	181 Tggtaccagcaagaacccaggagcagctctcttaacctgcatctactggtgcatccactag	DEFINITION 602571534P1 NIH_MGC_77 Homo sapiens CDNA clone IMAGE:4695873 5',	78.2%	416	66
Db	211 TGGTACACAGCAAGAACACGAGACGGCTCTTAAGTGTGCATATTACTGGGCAATCTACCGG	ACCESSION BGS42772	0	83	4
Db	241 gaattgggtgtccctgcatcgcttcaagtgtgagttgatactggagcatcttactcacc	KEYWORDS BGS42772.1 GI:13535005	83	Indels	4
Db	271 GAATCCGGGGGTCCTCCAGACGATTCAGTGTGGACGGGGTCTGGACGATTTTCATCTCCACG	ORGANISM human.	83	Indels	4
Db	301 atccagcagctctcaagctcgaagaacgtggcagtttatctgcaacgaactctat--tat	REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	83	Indels	4
Db	331 ATTCACAGAGCTTCAGAGCTGAAGATGTGCGAGTTTATTACTGTGCACAAATATTATAGTACT	AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	83	Indels	4
Db	358 cttaacagcttcgagcaagggagcaaggtggaataa 396	TITLE NIH-MGC http://mgi.nci.nih.gov/.	83	Indels	4
Db	391 CCTCAGACGTTCCGACCAAGGACCAAGGTGGAATCAAA 429	JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)	83	Indels	4
Db	151 ATCAACTGCAAGTCCAGACGAGAGTCTTTATACACTCCACAAATAGACTACTTTCT	COMMENT Unpublished (1999)	83	Indels	4
Db	181 Tggtaccagcaagaacccaggagcagctctcttaacctgcatctactggtgcatccactag	CONTACT Robert Strausberg, Ph.D.	83	Indels	4
Db	211 TGGTACACAGCAAGAACACGAGACGGCTCTTAAGTGTGCATATTACTGGGCAATCTACCGG	Email: cgapbs-remail.nih.gov	83	Indels	4
Db	241 gaattgggtgtccctgcatcgcttcaagtgtgagttgatactggagcatcttactcacc	Tissue Procurement: Clontech Laboratories, Inc.	83	Indels	4
Db	271 GAATCCGGGGGTCCTCCAGACGATTCAGTGTGGACGGGGTCTGGACGATTTTCATCTCCACG	CDNA Library Preparation: Clontech Laboratories, Inc.	83	Indels	4
Db	301 atccagcagctctcaagctcgaagaacgtggcagtttatctgcaacgaactctat--tat	DNA Sequencing by: Incyte Genomics, Inc.	83	Indels	4
Db	331 ATTCACAGAGCTTCAGAGCTGAAGATGTGCGAGTTTATTACTGTGCACAAATATTATAGTACT	Clone distribution: MGC clone distribution information can be	83	Indels	4
Db	358 cttaacagcttcgagcaagggagcaaggtggaataa 396	found through the I.M.A.G.E. Consortium/LLNL at:	83	Indels	4
Db	391 CCTCAGACGTTCCGACCAAGGACCAAGGTGGAATCAAA 429	http://image.llnl.gov	83	Indels	4
Db	151 ATCAACTGCAAGTCCAGACGAGAGTCTTTATACACTCCACAAATAGACTACTTTCT	Plate: L10M1522 row: C column: 10	83	Indels	4
Db	181 Tggtaccagcaagaacccaggagcagctctcttaacctgcatctactggtgcatccactag	High quality sequence stop: 615.	83	Indels	4
Db	211 TGGTACACAGCAAGAACACGAGACGGCTCTTAAGTGTGCATATTACTGGGCAATCTACCGG	Location/Qualifiers	83	Indels	4
Db	241 gaattgggtgtccctgcatcgcttcaagtgtgagttgatactggagcatcttactcacc	1. 633	83	Indels	4
Db	271 GAATCCGGGGGTCCTCCAGACGATTCAGTGTGGACGGGGTCTGGACGATTTTCATCTCCACG	/organism="Homo sapiens"	83	Indels	4
Db	301 atccagcagctctcaagctcgaagaacgtggcagtttatctgcaacgaactctat--tat	/db_xref="taxon:9606"	83	Indels	4
Db	331 ATTCACAGAGCTTCAGAGCTGAAGATGTGCGAGTTTATTACTGTGCACAAATATTATAGTACT	/clone="IMAGE:4695873"	83	Indels	4
Db	358 cttaacagcttcgagcaagggagcaaggtggaataa 396	/clone_lib="NIH_MGC_77"	83	Indels	4
Db	391 CCTCAGACGTTCCGACCAAGGACCAAGGTGGAATCAAA 429	/lab_host="DH10B (T1 phage-resistant)"	83	Indels	4
Db	151 ATCAACTGCAAGTCCAGACGAGAGTCTTTATACACTCCACAAATAGACTACTTTCT	/note="Organ: lung; Vector: pMNR-LIB (Clontech); Site: 1:	83	Indels	4
Db	181 Tggtaccagcaagaacccaggagcagctctcttaacctgcatctactggtgcatccactag	Site: 2: SfiI (ggccattatggc); 5' and	83	Indels	4
Db	211 TGGTACACAGCAAGAACACGAGACGGCTCTTAAGTGTGCATATTACTGGGCAATCTACCGG	3' adaptors were used in cloning as follows: 5' adaptor	83	Indels	4
Db	241 gaattgggtgtccctgcatcgcttcaagtgtgagttgatactggagcatcttactcacc	sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor sequence:	83	Indels	4
Db	271 GAATCCGGGGGTCCTCCAGACGATTCAGTGTGGACGGGGTCTGGACGATTTTCATCTCCACG	5'-ATTCTAGAGCGCCGCGCCGACATG-dT(30)BN-3' (where B = A,	83	Indels	4
Db	301 atccagcagctctcaagctcgaagaacgtggcagtttatctgcaacgaactctat--tat	C, or G and N = A, C, G, or T). Average insert size 1.9	83	Indels	4
Db	331 ATTCACAGAGCTTCAGAGCTGAAGATGTGCGAGTTTATTACTGTGCACAAATATTATAGTACT	kb (range 0.5-4.0 kb). 12/15 colonies contained inserts	83	Indels	4
Db	358 cttaacagcttcgagcaagggagcaaggtggaataa 396	by PCR. This library was enriched for full-length clones	83	Indels	4
Db	391 CCTCAGACGTTCCGACCAAGGACCAAGGTGGAATCAAA 429	and was constructed by Clontech Laboratories (Palo Alto,	83	Indels	4
Db	151 ATCAACTGCAAGTCCAGACGAGAGTCTTTATACACTCCACAAATAGACTACTTTCT	CA). Note: this is a NIH_MGC Library."	83	Indels	4
Db	181 Tggtaccagcaagaacccaggagcagctctcttaacctgcatctactggtgcatccactag		83	Indels	4
Db	211 TGGTACACAGCAAGAACACGAGACGGCTCTTAAGTGTGCATATTACTGGGCAATCTACCGG		83	Indels	4
Db	241 gaattgggtgtccctgcatcgcttcaagtgtgagttgatactggagcatcttactcacc		83	Indels	4
Db	271 GAATCCGGGGGTCCTCCAGACGATTCAGTGTGGACGGGGTCTGGACGATTTTCATCTCCACG		83	Indels	4
Db	301 atccagcagctctcaagctcgaagaacgtggcagtttatctgcaacgaactctat--tat		83	Indels	4
Db	331 ATTCACAGAGCTTCAGAGCTGAAGATGTGCGAGTTTATTACTGTGCACAAATATTATAGTACT		83	Indels	4



for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT 194 a 242 c 201 g 182 t  
ORIGIN

Query Match 62.5%; Score 247.6; DB 10; Length 819;  
Best Local Similarity 78.1%; Pred. No. 1.4e-65;  
Matches 311; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 1 atgagttcacagagccaggcttctatatatgctgctgctatggtatctggacacctgtgg 60  
DB 6 ATGCTGTTCAGAGCCAGCTCTTCAATTCCTGTGCTGTGATCTCTGTCCTACGGG 65  
QY 61 gacattgtgctgagacagatctccaatctccctgctgttaagcttagagagagggccact 120  
DB 66 GACGTCGTGTGACCCAGCTCCAGACTCCCGCTGTGTCTCTGTGGCGAGAGGGCCACC 125  
QY 121 attaactgcaaatccagctcagctcgtctcaacagtagaacccgagagaaactactgtgt 180  
DB 126 ATCAACTGCAGAGTCCAGCCAGAGGTGTTTATACAGCTCCAAATGATAGAACTTCTTAGCT 185  
QY 181 tggtaaccagcagaacccagggcagctctcctaaactgctgatactactggtgcatccactagg 240  
DB 186 TGGTACCACTGAAACACAGAGACGCTCTTAACATCACTTACTGCGCATCTACCCGG 245  
QY 241 gaattctgggtgctccctgcatcgtctcaagtgagtgatctggagacagattcactctcacc 300  
DB 246 GAATCCGGGGTCCCTGCGCTTTCAGTGGCACTGGTGTGGAGCAAGATTTCCTCTCACCC 305  
QY 301 atcagcagctcagcagctgaaagcgtgcaagtttacttactgacccaatctataat--- 357  
DB 306 ATCAGCAGCTCAGAGCTGGAAGATGTGGCAATTATTTCTGTACCAATATCATACTTCC 365  
QY 358 cttaacagctcgagacagggagccaagtgtaataaa 395  
DB 366 CCTGGACATTCGGCCAGAGGACCAAGGTGGAATCAA 403

RESULT 15  
BG757770 842 bp mRNA linear EST 15-MAY-2001  
LOCUS 602714882F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4854885 5',  
DEFINITION mRNA sequence.  
ACCESSION BG757770  
VERSION BG757770.1 GI:14068423  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 842)  
AUTHORS NIH-MGC htlp://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCMT/03 row: d column: 22  
High quality sequence stop: 736.

FEATURES  
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location/Qualifiers  
1. .842  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

/clone="IMAGE:4854885"  
/clone\_lib="NIH\_MGC\_48"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: B-cells; Vector: pORF7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(C). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC library."

BASE COUNT 197 a 247 c 207 g 191 t  
ORIGIN

Query Match 62.5%; Score 247.6; DB 10; Length 842;  
Best Local Similarity 78.1%; Pred. No. 1.4e-65;  
Matches 311; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 1 atgagttcacagagccaggcttctatatatgctgctgctatggtatctggacacctgtgg 60  
DB 6 ATGCTGTTCAGAGCCAGAGTCTTCAATTCCTGTGCTGTGATCTCTGTCCTACGGG 65  
QY 61 gacattgtgctgagacagatctccaatctccctgctgttaagcttagagagagggccact 120  
DB 66 GACGTCGTGTGACCCAGCTCCAGACTCCCGCTGTGTCTCTGTGGCGAGAGGGCCACC 125  
QY 121 attaactgcaaatccagctcagctcgtctcaacagtagaacccgagagaaactactgtgt 180  
DB 126 ATCAACTGCAGAGTCCAGCCAGAGGTGTTTATACAGCTCCAAATGATAGAACTTCTTAGCT 185  
QY 181 tggtaaccagcagaacccagggcagctctcctaaactgctgatactactggtgcatccactagg 240  
DB 186 TGGTACCACTGAAACACAGAGACGCTCTTAACATCACTTACTGCGCATCTACCCGG 245  
QY 241 gaattctgggtgctccctgcatcgtctcaagtgagtgatctggagacagattcactctcacc 300  
DB 246 GAATCCGGGGTCCCTGCGCTTTCAGTGGCACTGGTGTGGAGCAAGATTTCCTCTCACCC 305  
QY 301 atcagcagctcagcagctgaaagcgtgcaagtttacttactgacccaatctataat--- 357  
DB 306 ATCAGCAGCTCAGAGCTGGAAGATGTGGCAATTATTTCTGTACCAATATCATACTTCC 365  
QY 358 cttaacagctcgagacagggagccaagtgtaataaa 395  
DB 366 CCTGGACATTCGGCCAGAGGACCAAGGTGGAATCAA 403

Search completed: August 26, 2002, 16:13:43  
Job time: 4337 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 16:19:48 ; Search time 266.46 Seconds

(without alignments)  
2551.595 Million cell updates/sec

Title: US-09-249-011-7

Perfect score: 396

Sequence: 1 atgattcacaggcccaaggt.....ggaccacagtggaataaaa 396

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq\_032802:\*

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2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.\*  
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22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	396	100.0	396	21	AAA59695
2	360.8	91.1	396	21	AAA59693
3	340	85.9	480	10	AAAN91663
4	332	83.8	952	16	AAO94036
5	301.4	76.1	439	18	AAT60729
6	301.4	76.1	439	18	AAT60730
7	298.2	75.3	399	15	AAO66845
8	293.6	74.1	402	18	AAT43415
9	288.6	72.9	399	17	AAO74067

10	288.6	72.9	439	18	AAT60734	CDNA encoding wild
11	286.8	72.1	418	17	AAT34152	Monoclonal antibody
12	285.4	72.1	439	18	AAT72268	Chimeric Mab 15 PC
13	285.4	72.1	460	18	AAT72238	Mouse Mab 15 light
14	283.2	71.5	342	20	AAK34465	Mouse Mab 6A4 light
15	279.8	70.7	1443	15	AAO62958	Glycophorin antbo
16	279	70.5	427	20	AAK32779	Murine monoclonal
17	279	70.5	8068	20	AAK32781	PKN100 F19 chimeri
18	278.6	70.4	748	21	AAZ28962	Human anti-glycoph
19	277.8	70.2	747	19	AAV36237	Human od ScFv D3M wh
20	275.8	69.6	870	15	AAO62956	Glycophorin antbo
21	275.2	68.4	660	14	AAO53430	Sequence encoding
22	270.8	68.4	330	19	AAV29839	Anti-DNA IL/TM (H2
23	270.6	68.3	864	20	AAV72072	Fusion protein PIC
24	270.6	68.3	2019	20	AAV72059	Plasmid pMG4/55.1s
25	270.6	68.3	2025	20	AAV72064	Fusion protein PNG
26	267.2	67.5	336	20	AAK34588	Mouse Mab 6A4 muta
27	267.2	67.5	1701	13	AAO30919	pmR1006 insert.
28	267.2	67.5	1701	13	AAO30920	Vector pmR1007.
29	264.4	66.8	404	22	AAE81911	Anti-CA125 bifunct
30	261.4	66.0	400	9	AAV80499	Encodes V region o
31	260.8	65.9	511	20	AAV86720	EST clone AY241.
32	257.4	65.0	398	15	AAO66699	DREG-200 Ab light
33	257.4	65.0	798	14	AAO34842	Encodes V kappa reg
34	253.2	64.4	423	20	AAK90025	Human monoclonal a
35	253.2	64.4	1033	22	AAK900145	Human CDNA clone H
36	253.6	64.0	463	21	AAK98443	Human colon cancer
37	250.2	63.2	407	13	AAO26047	V-region of L-chain
38	248.6	62.8	402	16	AAT00780	E-selectin-specifi
39	248.6	62.8	8068	20	AAK32784	PKN100 human resha
40	248.2	62.7	344	13	AAO30900	Insert pmR1003.
41	247	62.4	5703	17	AAT34110	Anti-IL-5 humanise
42	247	62.4	5703	19	AAV03504	Plasmid pCNI15H2LC
43	244.8	61.8	744	20	AAK77243	Mouse scFv fragmen
44	244.8	61.8	774	24	AAK97144	P5-23 single chain
45	244.8	61.8	1515	24	AAK97148	3B10xP5-23 bispect

## ALIGNMENTS

RESULT 1	
AAA59695	standard; DNA: 396 BP.
AC	AAA59695;
XX	
DT	14-NOV-2000 (first entry)
XX	
DE	DNA encoding light chain variable region of humanised 3S1 antibody.
XX	
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW	autoimmune disease; infectious disease; inflammatory disorder;
KW	systemic lupus erythematosus; diabetes mellitus; insulinitis; asthma;
KW	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW	multiple sclerosis; transplant rejection; proliferative disease;
KW	leukemia; lymphoma; anemia; sickle-cell anemia; thalassemia;
KW	aplastic anaemia; myeloid dysplasia syndrome; ss.
XX	
OS	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
FT	
FT	key
FT	CDS
FT	Location/Qualifiers
FT	1..396
FT	/*tag= a
FT	/product= "light chain variable region of 3D1 antibody"
FT	/note= "no termination codon given"
FT	1..60
FT	/*tag= b
FT	mat_peptide
FT	61..396
FT	/*tag= c
XX	

PN MO200047625-A2.  
 PD 17-AUG-2000.  
 XX  
 PE 09-FEB-2000; 2000OWO-US03303.  
 XX  
 PR 12-FEB-1999; 990US-0249011.  
 PR 24-JUN-1999; 990US-0339596.  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;  
 PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;  
 XX  
 DR WPI; 2000-524532/47.  
 DR P-PSDB; AAB07966.  
 XX  
 PT Humanized immunoglobulin having a binding specificity to B7-1 (derived  
 PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12542) molecules,  
 PT modulates immune responses and can therefore treat e.g. autoimmune  
 PT diseases, infectious diseases -  
 XX  
 PS  
 XX Example 3; Fig 2B; 162pp; English.  
 XX  
 CC The present sequence encodes the light chain variable region of the  
 CC humanized murine antibody 3D1. The antibody has a binding specificity to  
 CC B7 molecules. The antibody is used to construct humanized  
 CC immunoglobulins, which comprise an antigen binding region of non-human  
 CC origin and a portion of a human immunoglobulin. The humanized  
 CC immunoglobulins are useful for treating autoimmune diseases, infectious  
 CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes  
 CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,  
 CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are  
 CC also useful for treating a transplant recipient and preventing transplant  
 CC rejection in a transplant recipient, and treating proliferative disease  
 CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,  
 CC thalassemia and aplastic anaemia), inborn errors of metabolism,  
 CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.  
 XX  
 Q0 Sequence 396 BP; 100 A; 96 C; 104 G; 96 T; 0 other;

Query Match	100.0%	Score 396:	DB 21:	Length 396:
Best Local Similarity	100.0%	Pred. No. 2.5e-119;		
Matches 396:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db 1 atggattccaaagcccaagcttcttatatgctgcgcgcgtatggglatctgcacccctggg 60				
QY 61 gacattctgctgaaacaagctcccaagatccctctgctgttaagctttgagagaagggccact 120				
Db 61 gacattctgcttcaacaagctcccaagatccctctgctgttaagctttgagagaagggccact 120				
QY 121 attagctgcaaaatcccaagctcagctctgtcccaacagttagaaccgcgagagaactcttggt 180				
Db 121 attagctgcaaaatcccaagctcagctcagctctgtcccaacagttagaaccgcgagagaactcttggt 180				
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Db 181 tggtaaccagcaaaaccagggcagcctctcctaaccgctgatactactgggcatccactaag 240				
QY 241 gaattctgggggtccctcgatcgccttcaagtgggcagttgatactgggaaccgaatttcactctcac 300				
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QY 301 atccagcaatctgcgaagcctggaagacgtctgcagcttatactgcagcgaactctataatctt 360				
Db 301 atccagcaatctgcgaagcctggaagacgtctgcagcttatactgcagcgaactctataatctt 360				
QY 361 tacacgtcttcggaaggggaaccaaggttggaataaana 396				
Db 361 tacacgtcttcggaaggggaaccaaggttggaataaana 396				

XX	RESULT	2
XX	AAA59693	standard; DNA; 396 BP.
XX	AAA59693	
XX	AAA59693;	
XX	14-NOV-2000	(first entry)
DE	Nucleotide sequence of light chain variable region of 3S1 antibody.	
XX		
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;	
KM	autoimmune disease; infectious disease; inflammatory disorder;	
KM	systemic lupus erythematosus; diabetes mellitus; insultitis; asthma;	
KM	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;	
KM	multiple sclerosis; transplant rejection; proliferative disease;	
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;	
KM	aplastic anaemia; myeloid dysplasia syndrome; ss.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..396
FT		/tag= a
FT		/product= "light chain variable region of 3D1 antibody"
FT		/note= "no termination codon given"
FT	sig_peptide	1..60
FT		/tag= b
FT	mat_peptide	61..396
FT		/tag= c
PN	WO20047625-A2.	
XX		
PD	17-AUG-2000.	
PF	09-FEB-2000; 2000WO-US03303.	
PR	12-FEB-1999; 99US-0249011.	
PR	24-JUN-1999; 99US-0339596.	
PA	(GENY ) GENETICS INST INC.	
PI	Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;	
PI	Gray GS, Knight A, O'hara D, Rup B, Veldman GM;	
XX		
DR	WPI: 2000-524532/47.	
DR	P-PSDB: AAB07964.	
PT	Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263) or B7-2 (derived from ATCC CRL-12524) molecules,	
PT	modulates immune responses and can therefore treat e.g. autoimmune diseases, infectious diseases -	
XX		
PS	Example 1; Fig 1B; 162pp; English.	
XX		
CC	The present sequence encodes the light chain variable region of the murine antibody 3D1. The antibody has a binding specificity to B7	
CC	molecules. The antibody is used to construct humanized immunoglobulins,	
CC	which comprise an antigen binding region of non-human origin and a	
CC	portion of a human immunoglobulin. The humanized immunoglobulins are	
CC	useful for treating autoimmune diseases, infectious diseases,	
CC	inflammatory disorders, systemic lupus erythematosus, diabetes	
CC	mellitus, insulinits, asthma, arthritis, inflammatory bowel disease,	
CC	inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are	
CC	also useful for treating a transplant recipient or preventing transplant	
CC	rejection in a transplant recipient, and treating proliferative disease	
CC	(leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,	
CC	thalassaemia and aplastic anaemia), inborn errors of metabolism,	
CC	congenital immunodeficiency diseases, and myeloid dysplasia syndrome.	
XX		
Sequence	396 BP; 98 A; 97 C; 104 G; 97 T; 0 other;	

XX	RESULT	2
XX	AAA59693	standard; DNA; 396 BP.
XX	AAA59693	
XX	AAA59693;	
XX	14-NOV-2000	(first entry)
DE	Nucleotide sequence of light chain variable region of 3S1 antibody.	
XX		
KW	Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;	
KM	autoimmune disease; infectious disease; inflammatory disorder;	
KM	systemic lupus erythematosus; diabetes mellitus; insultitis; asthma;	
KM	arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;	
KM	multiple sclerosis; transplant rejection; proliferative disease;	
KW	leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;	
KM	aplastic anaemia; myeloid dysplasia syndrome; ss.	
OS	Mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..396
FT		/tag= a
FT		/product= "light chain variable region of 3D1 antibody"
FT		/note= "no termination codon given"
FT	sig_peptide	1..60
FT		/tag= b
FT	mat_peptide	61..396
FT		/tag= c
PX		
PN	WO20047625-A2.	
XX		
PD	17-AUG-2000.	
PX		
PF	09-FEB-2000; 2000WO-US03303.	
XX		
PR	12-FEB-1999; 99US-0249011.	
PR	24-JUN-1999; 99US-0339596.	
XX		
PA	(GENY ) GENETICS INST INC.	
PI	Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;	
PI	Gray GS, Knight A, O'hara D, Rup B, Veldman GM;	
XX		
DR	WPI: 2000-524532/47.	
DR	P-PSDB; AAB07964.	
PT	Humanized immunoglobulin having a binding specificity to B7-1 (derived from ATCC PTA-263) or B7-2 (derived from ATCC CRL-12524) molecules,	
PT	modulates immune responses and can therefore treat e.g. autoimmune diseases, infectious diseases -	
XX		
PS	Example 1; Fig 1B; 162pp; English.	
XX		
CC	The present sequence encodes the light chain variable region of the murine antibody 3D1. The antibody has a binding specificity to B7	
CC	molecules. The antibody is used to construct humanized immunoglobulins,	
CC	which comprise an antigen binding region of non-human origin and a	
CC	portion of a human immunoglobulin. The humanized immunoglobulins are	
CC	useful for treating autoimmune diseases, infectious diseases,	
CC	inflammatory disorders, systemic lupus erythematosus, diabetes	
CC	mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,	
CC	inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are	
CC	also useful for treating a transplant recipient or preventing transplant	
CC	rejection in a transplant recipient, and treating proliferative disease	
CC	(leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,	
CC	thalassaemia and aplastic anaemia), inborn errors of metabolism,	
CC	congenital immunodeficiency diseases, and myeloid dysplasia syndrome.	
XX		
Sequence	396 BP; 98 A; 97 C; 104 G; 97 T; 0 other:	



PA (ZENEC) ZENEC LTD.  
 XX  
 PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;  
 PI Rose MS, Wright AF;  
 XX  
 DR WPI: 1995-215262/28.  
 DR P-PSDB: AAR76087.  
 XX  
 PT Antigen binding structures containing CDRs recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the  
 PT diagnosis and therapy of cancer  
 XX  
 PS  
 PS Disclosure: Fig.16; 121pp; English.  
 XX  
 CC Mab 55.1 (ECACC 93081901) recognises the colorectal tumor-associated  
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)  
 CC chains of 55.1 were isolated, and F(ab)'<sub>2</sub>, Fab, Fv, scFv or  
 CC V-chain humanised 55.1 constructs have been expressed in myeloma  
 CC cells and E. coli.  
 XX  
 XQ Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;

Query Match	83.8%	Score 332	DB 16	Length 952
Best Local Similarity	89.9%	Pred. No. 2.9e+8		
Matches 356; Conservative	0;	Mismatches 40;	Indels 0;	Gaps 0;

QY	1	atgatatcaacaggccccaaggtttcttatattgtctgtctgtatagggatctctgacacctgtgg	60
Db	16	atggattcaacaggccccaaggtttcttatattgtctgtctgtatagggatctctgacacctgtgg	75
QY	61	gaactgtgcgcgacacagctctccagatctccctgtgctgtaagcttagagagagggccaact	120
Db	76	gaactgtgtgattgtacaacgtctctccatctctccctgtgctgtgtcagcagagagagggccaac	135
QY	121	atcagctgcacaaatccagatcagatctgtctcacaacagtagaaccggagagaaactactgtgct	180
Db	136	atgagcgtgcacaaatccagatcagatctctcctcaacagtagaaccggagagaaactactgtgct	195
QY	181	tgtgtacccagcagaaaccagaagcagcctctcctaaactgtgtgtatctacatctggtgagatccactaag	240
Db	196	tgtgtacccagcagaaaccagaagcagcctctcctcctaaactgtgtgtatctacatctggtgagatccactaag	255
QY	241	gaatctgagggctccctgtatctgctgttaagtgtgcagctgtgatactgagacagattccactccacc	300
Db	256	acatctgaggggtccctgtatctgctgttaacacagcagctgtgatactggtgagacagattccactccacc	315
QY	301	atcagcagatctgcagagcttgaagacgtgtggcagtttatatctacatgcacgcaatcttaactctt	360
Db	316	atcagcagatctgcagagcttgaagacgtgtgaatcttatattacatctgcacgcaatcttaactctt	375
QY	361	tacacgttctgcgacagcagggacccaaggtgtgaataataa	396
Db	376	cgaacgttctgcgttgcgtaggcacacaaagctgtgaataataa	411

RESULT	5
AAT60729	
ID	AAT60729 standard; cDNA; 439 BP.
XX	
AC	AAT60729;
XX	
DT	25-SEP-1997 (first entry)
XX	
DE	cDNA encoding humanised murine anti-E-selectin antibody C17188v(1A)
XX	
KW	Humanised; murine; mouse; E-selectin; antibody; light chain;
KW	variable region; detection; inhibition; mediation; cell adhesion;
KW	diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;
KW	acute respiratory distress syndrome; gross cystic breast disease;
KW	cancer; treatment; splanchnic occlusion shock; psoriasis;
XX	complement; chimeric; ds.
XX	

OS	Chimeric - Mus spp.		
OS	Chimeric - Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	16..426	
FT		/**tag= a	
FT		/note= "no stop codon given"	
XX			
PN	WO9640942-A1.		
XX			
PD	19-DEC-1996.		
XX			
PE	06-JUN-1996;	96WO-US09204.	
XX			
PR	07-JUN-1995;	95US-0482112.	
XX			
PA	(CYTE-) CYTEL CORP.		
XX			
PI	Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;		
PI	Jones S;		
XX			
DR	WPI: 1997-077272/07.		
DR	P-PSDB; AAM10544.		
XX			
PT	Humanised anti-E-selectin antibody - useful for diagnosis and		
PT	treatment of, e.g. inflammatory responses, septic shock, acute		
PT	respiratory distress syndrome or cancer		
XX			
PS	Claim 29; Page 69; 89pp; English.		

CC The present sequence encodes the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, C11788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, gross cystic breast disease or cancer, or treat, e.g.  
CC splenic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.

Query Match	Score	DB	Length
Best Local Similarity	76.18;	301.4;	439;
Matches 345; Conservative	86.58;	Pred. No. 2.1e-88;	
	0;	Mismatches 51;	Indels 3; Gaps 1;

Oy	1	atgattcaacagcgcccaaggtctctatatctgtctgtgctatgggtatctggaaccttggg	60
Db	28	atgagatcaacagctctccaggtccctccatgacgccccgtgtctctcgggtatccctgtacctgtgg	87
Oy	61	gacctgtgtctgtaacacagctctccagatctccctgtgctgtaaagctbagagagagggccact	120
Db	88	gaccttgtgatatgaacagctccccaagactccctgtgctgtgtctctgtgacgagagggccacc	147
Oy	121	attgagctgcacaatccatccataagctctgtctcaacagctagaagcccgagagaactactgtgct	180
Db	148	atcaacctgcagaagctccagctcagctgtcttacaagctgtgaaatcaaaaagaactacttgacc	207
Oy	181	tgtgtaccagcgagaacacgaagcgagcctctctaaactgtgtactgtactgtgacatccactaagg	240
Db	208	tgtgtaccagcgagaacacgaagcgagcctctctaaactgtgtactgtactgtgacatccactaagg	267
Oy	241	gaactctgggtgacctgtgctgttcgaatgtggcagctgagatctcgggacagattccactccacc	300
Db	268	gaactctgggtgacctgtgctgttcgaatgtggcagctgagatctcgggacagattccactccacc	327
Oy	301	atcagcagactctgcaggtctgtaagacgtgtgcagttatctatctgcaogcaactctata---at	357
Db	328	atcagcagactctgcaggtctgtaagacgtgtgcagttatctatctgcaogcaatgataatctat	387



CC deduced AA sequences are shown in AAQ66845/R59509 and AAQ66846/R59510  
XX  
SQ Sequence 399 BP; 102 A; 88 C; 100 G; 109 T; 0 other;

Sequence 399 BP; 102 A; 88 C; 100 G; 109 T; 0 other;

Query Match	75.3%	Score 298.2	DB 15	Length 399
Best Local Similarity	86.0%	Pred. No. 2.3e-87		
Matches 343	Conservative	0	Mismatches 53	Indels 3
				Gaps 1

QY	1	atggaatcaacagcgcccaaggtctctatatatttgctgtgtctatgagatcttgcacctgtggg	60
Db	1	atggaatcaacagcgcccaaggtctctatatatttgctgtgtctatgagatcttgcacctgtggg	60
QY	61	gacattgtgtctgcacacagctctccagatctcccttggctctgtaagctttagagagagagggccact	120
Db	61	gacattgtgtgtatccacagctctccatccatccctccttagctgtgtaagctttagagagagagggctact	120
QY	121	attgactctgcacaaatcccaagtcagagctctgtctctcaacagatagaaccggagagaaactacttgct	180
Db	121	atgagctctgaagctccagatccagatcagagcctcttataatagtagcatctcaaaagaattacttggcc	180
QY	181	tgtgtaaccgacgagaaaccagggcgagcctccctaaactgtgtgtactgtgtggtatccacatagg	240
Db	181	tgtgtaaccgacgagaaaccagggcgagcctccctaaactgtgtgtactgtgtggtatccatcaacagg	240
QY	241	gaatctgtagggccctctgatacgtcttcagctgtgacgtgagatctcgagacagatttccactctacc	300
Db	241	gaatctgtagggccctctgatacgtcttcacacggcgacgtgagatctcgtagacagatttccactctacc	300
QY	301	atcagcagctctgcacagcgctgtgaagacgtgtgcagtttatattactgtcacgcgaactctata--at	357
Db	301	atcagcagctgtgaaagcgctgaagacccctgtgcagtttatattactgtcacgaactatataagctat	360
QY	358	ctttacaacgcttcggaacaggggagccaagaagtgtgaataataa	396
Db	361	ccattcacagcttgcgctctggtgtgagacaagaatttggaaataataa	399

RESULT	8
AAAT43415	
ID	AAAT43415 standard; cDNA to mRNA; 402 BP.
XX	
AC	AAAT43415;
XX	
DT	17-FEB-1997 (first entry)
XX	
DE	Xenograft antibody HAR-1 light chain variable region cDNA.
XX	
KW	Xenograft rejection; xenotransplantation; organ transplant;
KW	animal model; hamster; monoclonal antibody; HAR-1; ds.
XX	
OS	Rattus sp.
XX	
FH	Key
FT	CDS
FT	1..402
FT	location/Qualifiers
FT	1..402
FT	/*tag= a
FT	/product= immunoglobulin variable region
FT	/standard_name= Ig kappa chain variable region
FT	/label= VK_Region
FT	/note= "HAR-1 kappa light chain variable region"
FT	1..60
FT	misc_RNA
FT	1..60
FT	/*tag= b
FT	/standard_name= Leader
FT	/label= Leader
FT	61..129
FT	misc_RNA
FT	61..129
FT	/*tag= c
FT	/standard_name= Framework region 1
FT	/label= FR-1
FT	/note= "framework region 1 of HAR-1 kappa light chain variable region"
FT	130..180
FT	misc_RNA
FT	130..180
FT	/*tag= d
FT	/standard_name= CDR-1

Query Match	Best Local Similarity	Score	DB	Length	402;
Matches 332; Conservative	74.1%; 83.8%; 0;	293.6; 7.3e-86; 64;	18;	402;	0; Gaps 0;

Query Match	74.1%	Score 293.6;	DB 18;	Length 402;
Best Local Similarity	83.8%;	Pred. No. 7.3e-86;		
Matches 332;	Conservative 0;	Mismatches 64;	Indels 0;	Gaps 0;

```

QY 1 atggattcacagggccggtcttatatgtctgtctatgtgtatctgacctgtgg 60
DB 1 atggaatcacagaacagggctccatccatgctcgtcgtcgtggtatctgttactgtgg 60
QY 61 gacattgtctgacacagctccagatctccctgtgctgtaagcttaagagaagagccact 120
DB 61 gacattgtgtagcaccagctccatctccatccagctgtgtcagcagggagaagagtcact 120
QY 121 attagctgaatccaagctagaagctgtctcaacagtagaacccagagaactactgtgct 180
DB 121 atgagctgcaagctcagctcagctcttattatacaatgaacaaagaactactgtgcc 180
QY 181 tgggtccagcaaaaacccaagggcagcctcctaactgtatctatctacgtgggcatccactag 240
DB 181 tggtagccgcagaaaacccaagggcagctcctaactgtatctacgtgggcatccactag 240
QY 241 gaatctgggtccctcatcgtctcaatggtgagtgatctcgtggcagatctcactacc 300
DB 241 gaatctgggtccctcatcgtctcaatggtgagtgatctcgtggcagatctcactacc 300
QY 301 atcagcagctctcagcagctgaaagcgtgcaatttacttactcagcgaactctataact 360
DB 301 atcagcagctgtagcagcagagaagacccgtgttattactgtcagcagactataactgt 360
QY 361 tacacgttcggacaggggacccaaggtggaataaaa 396
DB 361 tacacgttcggagctgggacccaagctggaactgaaa 396

RESULT 9
AA074067
ID AA074067 standard; DNA; 399 BP.
AC
XX AA074067;
XX
DT 02-JUL-1996 (first entry)
XX
DE Monoclonal antibody, CB-Hep.1, light chain variable domain cDNA.
XX
KW HBV; hepatitis B virus surface antigen; monoclonal; antibody;
KW CB-Hep.1; immunopurification; detection; hybridoma; recombinant; Fv;
KW variable; VH; HBSAg; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..399
FT sig_peptide /tag= a
FT mat_peptide /tag= b
FT misc_feature /tag= c
FT misc_feature /tag= d
FT misc_feature /tag= FR1
FT misc_feature /tag= e
FT misc_feature /label= CDR1
FT misc_feature /tag= f
FT misc_feature /label= FR2
FT misc_feature /tag= g
FT misc_feature /label= CDR2
FT misc_feature /tag= h
FT misc_feature /label= FR3
FT misc_feature /tag= i
FT misc_feature /label= CDR3
FT misc_feature /tag= j
FT misc_feature /label= FR4

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XX EP686696-A1.
PN 13-DEC-1995.
PD 09-JUN-1995; 95EP-0201535.
PE 09-JUN-1994; 94CU-0000073.
PR (ING-) CENT ING GENETICA & BIOTECNOLOGIA.
PA (KAMB/) KAMBEEL R W.
XX
PI Ayala Avila MA, Canaan-Haden Frias LM, del Carmen Dominguez Horta MC;
PI Fernandez de Cossio Dorta-Duque ME, Gavilondo Cowley JVG;
DR MPI; 1996-021914/03.
DR P-PSDB; AAR85909.
XX
PT New recombinant single chain Fv antibody fragment - useful for
PT Immuno-purificn. and detection of HBSAg
XX
PS Claim 1; Page 19; 23pp; English.
XX
CC AA074066 and AA074067 encode the heavy and light chain variable domains
CC of the murine hybridoma-derived monoclonal antibody CB-Hep.1 Fv region.
CC The heavy and light chain regions are used to produce a recombinant
CC antibody fragment having specificity for the hepatitis B virus
CC surface antigen (HBSAg). The recombinant antibody may be used for
CC immunopurification of HBSAg, in immunoassays for the detection of
CC HBSAg and for insolubilisation of heterologous fusion proteins
CC expressed in E. coli aiding their purification.
XX
SQ Sequence 399 BP; 98 A; 88 C; 101 G; 112 T; 0 other;

Query Match 72.9%; Score 288.6; DB 17; Length 399;
Best Local Similarity 84.5%; Pred. NO. 3.1e-84;
Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;

QY 1 atgattcacagggccaggtcttatatgtctgtctgctatggtgtatctggcactgtgg 60
DB 1 atgattcacagggccaggtcttatatgtctgtctgctatggtgtatctggcactgtgg 60
QY 61 gacattgtctgacacagctccagatctccctgtgctgtaagcttaagagaagagccact 120
DB 61 gacattgtgtagcaccagctccatctccatccatcgtgtgtcagcttggaagagtgct 120
QY 121 attagctgaatccaagctagaagctgtctcaacagtagaacccagagaactactgtgct 180
DB 121 atgagctgcaagctcagctcagctcttattatacaatgaacaaagaactactgtgcc 180
QY 181 tggtagccagagaacccaagggcagcctcctaactgtgtaactcagtcagtcactag 240
DB 181 tggtagccagagaacccaagggcagctcctaactgtgtaactcagtcagtcactag 240
QY 241 gaatctgggtccctcatcgtctcaatggtgagtgatctcgtggcagatctcactacc 300
DB 241 gattctgggtccctcatcgtctcaatggtgagtgatctcgtggcagatctcactacc 300
QY 301 atcagcagctctcagcagctgaaagcgtgcaatttacttactcagcgaactctata 357
DB 301 atcagcagctgtagaagctggaagccctggcaggttattactcagcaacataataat 360
QY 358 cttaacgtctcgacaggggacaaagtgaataaaa 396
DB 361 cgttacagcttcggaggggagaccaagctggaataaaa 399

RESULT 10
AAT60734
ID AAT60734 standard; cDNA; 439 BP.
AC AAT60734;

```

XX 25-SEP-1997 (first entry)  
 DT CDNA encoding wild type murine anti-E-selectin antibody CY1787V(L).  
 XX  
 DE  
 XX Humanised; murine; mouse; E-selectin; antibody; light chain;  
 KM variable region; detection; inhibition; mediation; cell adhesion;  
 KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
 KM acute respiratory distress syndrome; gross cystic breast disease;  
 KM cancer; treatment; splanchic occlusion shock; psoriasis;  
 XX complement; ds.  
 XX  
 OS Mus spp.  
 FH  
 FH Key Location/Qualifiers  
 FT CDS 16..426  
 FT /tag= a  
 FT /note= "no stop codon given"  
 FT  
 XX WO9640942-A1.  
 PN 19-DEC-1996.  
 XX  
 PD 06-JUN-1996: 96WO-US09204.  
 XX  
 PE 07-JUN-1995: 95US-0482112.  
 XX  
 PR (CYTE-) CYTEL CORP.  
 XX  
 PA Bently MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
 PI Jones S;  
 XX  
 PI WPI: 1997-077272/07.  
 DR P-PSDB: AAM10547.  
 XX  
 XX Humanised anti-E-selectin antibody - useful for diagnosis and  
 PT treatment of, e.g. inflammatory responses, septic shock, acute  
 PT respiratory distress syndrome or cancer  
 FT  
 FT  
 PS Example II: Page 55; 89pp; English.  
 XX  
 CC The present sequence encodes the wild type murine anti-E-selectin  
 CC antibody (Ab) light chain variable region, CY1787V(L), which was  
 CC used in the preparation of the humanised anti-E-selectin Ab 119ht  
 CC chain variable regions, CY1788V(LA-B). The humanised Ab can  
 CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
 CC adhesion. They can also be used to diagnose, reduce or inhibit an  
 CC inflammatory response, or the severity of pathologies, e.g. septic  
 CC shock, acute respiratory distress syndrome, wound associated  
 CC sepsis, gross cystic breast disease or cancer, or treat, e.g.  
 CC splanchic occlusion shock, or psoriasis. They can be administered  
 CC to a human without inducing an immune response, in addition, the  
 CC effector portion of the Ab can interact with various components of  
 CC the human immune system, including complement.  
 CC  
 XX Sequence 439 BP; 108 A; 110 C; 116 G; 105 T; 0 other:  
 SQ  
 Query Match 72.9%; Score 288.6; DB 18; Length 439;  
 Best Local Similarity 84.5%; Pred. No. 3.2e-84;  
 Matches 337; Conservative 0; Mismatches 59; Indels 3; Gaps 1;  
 QY 1 atgagatcagagccaggtctctatattgtctgtcgtatcgtgacctgtgg 60  
 DB 28 atgagatcagagccaggtctctatattgtctgtcgtatcgtgacctgtgg 87  
 QY 61 gacattgtctgacacagctccagattccctgtgttaagcttagagagagccact 120  
 DB 88 gacattgtgtgacacagctccagattccctgtgttaagcttagagagagccact 147  
 QY 121 attagatgcaaatcagctcagatcgtcgtcagatagagaccgagagagactctggc 180  
 DB 148 atgagctgcaagatcagctcagatcgtcgtcagatagagaccgagagagactctggc 207

QY 181 tggtaaccagagaaccagagccctctaaactgtctgattactactggtgcatccactagg 240  
 DB 208 tggtaaccagagaaccagagccctctaaactgtctgattactactggtgcatccactagg 267  
 QY 241 gaactcgtggtccctgtatcgtcgtcagatgagatgagatcgtggagaaattcactccacc 300  
 DB 268 gaactcgtggtccctgtatcgtcgtcagatgagatgagatcgtggagaaattcactccacc 327  
 QY 301 atcagcagctcgtcagatgagagcgtgcaatttactactgacagcaattccta--at 357  
 DB 328 atcagcagctcgtcagatgagagcgtgcaatttactactgacagcaattcctaattat 387  
 QY 358 cttaacagcttcggaagagagccagaggtggaataaaa 396  
 DB 388 ccgctcagctcgtcgtcgtgagacaaagtgtgagctgaaa 426  
 RESULT 11  
 AAT34152  
 ID AAT34152 standard; DNA; 418 BP.  
 XX  
 AC AAT34152;  
 XX  
 DT 14-FEB-1997 (first entry)  
 XX  
 DE Monoclonal antibody PA1-3F10 variable light chain-encoding DNA.  
 XX  
 KM PA1-3F10: antibody; hybridoma; LMBP1322CB; cancer; target; epitope;  
 KM killing; colorectal; lung; ovary; cytotoxin; neoplasia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH  
 FH Key Location/Qualifiers  
 FT CDS 2..418  
 FT /tag= a  
 FT /note= "no start or stop codon"  
 FT  
 XX WO9622310-A1.  
 PN 25-JUL-1996.  
 XX  
 PD 15-JAN-1996: 96WO-SE00029.  
 XX  
 PE 18-JAN-1995: 95SE-0000148.  
 XX  
 PR (BIOT-) BIOINVENT INT AB.  
 XX  
 PA Carlsson R, Jansson B;  
 PI  
 XX WPI: 1996-354478/35.  
 DR P-PSDB: AAR99469.  
 XX  
 XX Monoclonal antibody PA1-3F10 produced by hybridoma BCCW LMBP1322CB -  
 PT useful to target cancer cells for killing or detection  
 FT  
 FT  
 PS Claim 10; Fig 10; 62pp; English.  
 XX  
 CC AAT34152 encodes the variable light (VL) chain of monoclonal antibody  
 CC PA1-3F10 produced by hybridoma BCCW LMBP1322CB. The antibody is  
 CC directed against an epitope present on cancer cells, in particular  
 CC breast, ovary, lung and colorectal cancer cells. The antibody is  
 CC useful for detecting cancer cell epitopes and hence in the diagnosis  
 CC of cancer. The antibody can be conjugated to a cytotoxic compound and  
 CC targeted to cancer cells to kill them.  
 CC  
 XX Sequence 418 BP; 102 A; 100 C; 107 G; 109 T; 0 other:  
 SQ  
 Query Match 72.4%; Score 286.8; DB 17; Length 418;  
 Best Local Similarity 84.8%; Pred. No. 1.2e-83;  
 Matches 334; Conservative 0; Mismatches 57; Indels 3; Gaps 1;







QY 241 gaatctgggtccctcgatcgttcagtgagtgatctcgggacagattcactcacc 300  
|||  
DB 181 gaatctgggtccctcgatcgttcacaggtgagtgatctcgggacagattcactcacc 240  
QY 301 atcagcagctgcagagctgaagacgttgagcttattactgacagcaattataatctt 360  
|||||  
DB 241 atcagcagctgcagagctgaagacgttgagcttattactgacagcaattataatctt 300  
QY 361 taacagcttcgacagaggaggaacaggttggaataaaa 396  
|||||  
DB 301 cggacgttcgtgagaggaacacgaagctggaataaaa 336

## RESULT 15

AA062958  
ID AA062958 standard; DNA; 1443 BP.

AA062958;

AC 09-SEP-1994 (first entry)

DE Glycophorin antibody 1C3 Fab coding region.

KW Glycophorin; antibody 1C3; target binding polypeptide; PCR;  
polymerase chain reaction; primer: antibody engineering;  
humanized antibody; phagemid pHF4; plasmid p569/ss.

OS Synthetic.

PN M09407921-A.

PD 14-APR-1994.

PE 24-SEP-1993; 93WO-A000491.

PR 25-SEP-1992; 92AU-0004973.

PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.

PI Atwell JL, Colman PM, Hudson PJ, Irving RA, Kortt A;  
Lah M, Malbyrl, Power BE;

DR WPI; 1994-135515/16.

PT New target-binding polypeptide(s) used for diagnosis, etc.  
PT Having a stable core polypeptide region with at least one  
PT target-binding region covalently attached, opt. mutated to alter  
PT specificity, etc.

PS Disclosure; Page 42; 67pp; English.

CC PCR primers given in AA062951-52 were used to clone anti-glycophorin  
CC antibody 1C3 Fab coding region. The DNA sequence of the first 1443  
CC bases of the Fab fragment in pHF4, ready for ligation post PCR  
CC amplification for ligation into p569, is given in AA062958.

XX Sequence 1443 BP; 391 A; 388 C; 351 G; 313 T; 0 other;

Query Match 70.7%; score 279.8; DB 15; Length 1443;  
Best Local Similarity 84.6%; Pred. No. 4e-81;  
Matches 314; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 26 tatgtctgtctatggtatcttgacacctgtgggacattgtctgacacagctccag 85  
|||  
DB 734 tcttacgcttactgttaccggtacccaagccgaactgctcatgtcacagcttccat 793

QY 86 attccctggtcgtgaagcttagagagagggccacattagctgcaaatccagtcagatc 145  
|||||  
DB 794 cctccctggtcgtgtagagagaggaagtctacattagctgacagatccagtcagatc 853

QY 146 tgcctcaagtagaacccgagagaactcttgctgtgtacacagagaacaggagcagc 205  
|||

DB 854 tgttcaacagtagaacccgaaagaacttgaacttggtaccagcagaacccagggcag 913  
QY 206 ctctaaactgctgatacttacttggtacatccactaggggaatctgggtccctgatacttca 265  
|||||  
DB 914 ctcttaaacgctgatacttacttggtacatccactaggggaatctgggtccctgatacttca 973  
QY 266 gtggcagtgatctgggacagatttcaacttcacacatcagcagctgcaggtgaagag 325  
|||||  
DB 974 caggcagtgatctgggacagatttcaacttcacacatcagcagtgctgcaagctgaagacc 1033  
QY 326 tggcagttattacttgacagcaatcttataatctttaaagcttcggagcaggaggaacaa 385  
|||||  
DB 1034 tggcagattattacttgacagcaatcttataatctttaaagcttcggagcaggaggaacaa 1093  
QY 386 tgggaataaaa 396  
|||||  
DB 1094 tgggaattaaa 1104

Search completed: August 26, 2002, 16:19:50  
Job time: 4484 sec





Db 190 TGGTACACAGAGACAGGAGGAGTCTCTAAACGTGATGATGGGATCCACTAGG 249  
Qy 241 gaattcggggtccctgattcgtctcaatgagtgatctcggagcaattcactccacc 300  
Db 250 ACATCTGGGGTCCCTGATGCTTCACAGGACAGTGATCTGGGACAAATTCACCTCCACC 309  
Qy 301 atcagcagctcgaagctgaagacgtgagcttattactgcagcgaattcacttaactc 360  
Db 310 ATCAGCAGTGTGACAGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTACTCTT 369  
Qy 361 tacagcttcgacagggaccaagtggaataaaa 396  
Db 370 CGAGCTTCGTGGAGGACACCAAGCTGGAATCAAA 405

RESULT 2  
US-08-929-856-65  
; Sequence 65, Application US/08929856  
; Patent No. 6136568

GENERAL INFORMATION:  
APPLICANT: Hatt, Andrew  
TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING  
NUMBER OF SEQUENCES: 190  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LERNER, DAVID, LITTEMBERG, KRUMHOLTZ &  
STREET: 600 South, Avenue West  
CITY: Westfield  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07090  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/929,856  
FILING DATE: 15-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Foley, Shawn P.  
REGISTRATION NUMBER: 33,071  
REFERENCE/DOCKET NUMBER: ROSE 3.0-057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-654-5000  
TELEFAX: 908-654-7866  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 342 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-08-929-856-65

Query Match 71.5%; Score 283.2; DB 3; Length 342;  
Best Local Similarity 90.2%; Pred. No. 6.2e-82;  
Matches 303; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 61 gacatttgctgaacagcttcacagattccctgctgcttaagcttaagagagagggccact 120  
Db 1 gacatttgctgaacagcttcacagattccctgctgcttaagcttaagagagagggccact 120  
Qy 121 attagctgcaaatcagctcagagctcgtctcaacagtagaacccgaggaactacttgct 180  
Db 1 attagctgcaaatcagctcagagctcgtctcaacagtagaacccgaggaactacttgct 180

Db 61 ATGAGTCGAATTCACGATGAGACTGTCTCAACAGTATTAACCGAAGAAGACTTCTGGCT 120  
Qy 181 tggtaacagcaagaacaaaggagcctccttaactctgattcactcaggagcattccactagg 240  
Db 121 TGGTACACAGAGAACACAGGAGGAGTCTCTAAACGTGATGATGGGATCCACTAGG 180  
Qy 241 gaattcggggtccctgattcgtctcaatgagtgatctcggagcaattcactccacc 300  
Db 181 GATCTGGGGTCCCTGATGCTTCACAGGACAGTGATCTGGGACAAATTCACCTCCACC 240  
Qy 301 atcagcagctcgaagctgaagacgtgagcttattactgcagcgaattcacttaactc 360  
Db 241 ATCAGCAGTGTGACAGCTGAAGACCTGGCAATTTATTACTGCAAGCAATCTTACTCTT 300  
Qy 361 tacagcttcgacagggaccaagtggaataaaa 396  
Db 301 CGAGCTTCGTGGAGGACACCAAGCTGGAATCAAA 336

RESULT 3  
US-08-403-853-19  
; Sequence 19, Application US/08403853  
; Patent No. 5844094

GENERAL INFORMATION:  
APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORR, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POWER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1443 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-853-19



APPLICATION NUMBER: US 07/983,949  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-45  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 399 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..399  
PCT-US93-11611-1

Query Match 70.1%; Score 277.4; DB 5; Length 399;  
Best Local Similarity 82.7%; Pred. No. 4,8e-80;  
Matches 330; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 atgattcacaagccagagcttctatattgctgctgctatggtatctgacacctgtg 60  
DB 1 ATGATTTCACAGGCCAGGTTCTTATGTACTGCTATGAGTATCGTAACCTGTGG 60  
QY 61 gacattgtctgacacagtcctcagattccctgctgttaagcttagagagagccact 120  
DB 61 GACATTGTATGTACAGAGTCTCCATCTCCCTAGCTGTGCACTTGAGAGAGGTACT 120  
QY 121 attagctgcaaatcagctgaagctctgctcaacagtagaacccagagaaactctggct 180  
DB 121 ATGAGCTGCAAGTCCAGTCAAGACCTTTTACTAGCTGTGTCAGATTGAGAGAGGTACT 180  
QY 181 tggtaacagacaagaacacagggcagcctcctaactctgatactactcgggacactag 240  
DB 181 TGGTACCAGACAGAAACAGGGCAGTCTCCTAACTGCTGATTACTGGGATCTACAGG 240  
QY 241 gaatctgggggtccctgattcgtctcagatgagcagtgatctgggacagatttcaccc 300  
DB 241 GAATCTGGGGTCCCTGATTCGCTTACACAGGCAGTGGGATCTGGGACAGATTTCACCTCACC 300  
QY 301 atcagagagctgcagagctgaagacgtgagcagttattactgacggaacttata--at 357  
DB 301 ATCAGCAGTGTGAAGGCTGGAAGACCTGGCAGTTATTACTGTACGCAATATTATACCTAT 360  
QY 358 ctttaacagcttcgacagggagaccaaagtggaataaaa 396  
DB 361 CCATTACGTTGGGCTCGGGGACAAAGTTGGAATAAAAA 399

RESULT 6  
US-08-403-853-15  
Sequence 15, Application US/08403853  
Patent No. 5844094

GENERAL INFORMATION:

APPLICANT: HUDSON, Peter J.  
APPLICANT: LAH, Maria  
APPLICANT: KORRT, Alex A.  
APPLICANT: IRVING, Robert A.  
APPLICANT: ATWELL, John L.  
APPLICANT: MALBY, Robyn L.  
APPLICANT: POMER, Barbara E.  
APPLICANT: COLMAN, Peter M.  
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,853  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/AU93/00491  
FILING DATE: 24-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PL 4973  
FILING DATE: 25-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16786/189/CHAC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ. ID NO. 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 870 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: mat.peptide  
LOCATION: 40..834  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 40..834  
US-08-403-853-15

Query Match 69.6%; Score 275.8; DB 2; Length 870;  
Best Local Similarity 89.0%; Pred. No. 2.1e-79;  
Matches 298; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 61 gacattgtctgacacagtcctcagattccctgctgttaagcttagagagagggcact 120  
DB 463 GACATTGTATGTACAGAGTCTCCATCTCCCTGCTGTGTCAGTAGAGAGAGTCACT 522  
QY 121 attagctgcaaatcagctgaagctctgctcaacagtagaacccagagaaactacttggct 180  
DB 121 ATGAGCTGCAAGTCCAGTCAAGTCTGTTCAACAGTAGAAGAACCGAAGAACTGAGT 582  
QY 181 tggtaacagacaagaacacagggcagcctcctaactctgatactactcgggacactag 240  
DB 181 TGGTACCAGACAGAAACAGGGCAGTCTCCTAAACCCGCTGATCTACCTGGGATCTAC 240  
QY 241 gaatctgggggtccctgattcgtctcagatgagcagtgatctgggacagatttcaccc 300  
DB 241 TGCTACACAGCAGAAACAGGGCAGTCTCCTAAACCCGCTGATCTACCTGGGATCTAC 300  
QY 241 gaatctgggggtccctgattcgtctcagatgagcagtgatctgggacagatttcaccc 300  
DB 643 GAATCTGGGGTCCCTGATTCGCTTACACAGGCAGTGGGATCTGGGACAGATTTCACCTCACC 702  
QY 301 atcagagcttcgacagctgaagacgtgagcagttattactgacgcaacttataactt 360  
DB 301 ATCAGCAGTGTGAAGGCTGGAAGACCTGGCAGTTATTACTGTACGCAAGCAATCTTATATCTT 762  
QY 361 tacacgttcgacagggagaccaaagtggaataaaa 395  
DB 763 CGAGCGTTGGTGGAGCACCAAGCTGGAATAATTA 797

RESULT 7  
US-08-957-001B-4



Sequence 4, Application US/08957001B  
Patent No. 6228621  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6228621ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/957,001B  
FILING DATE: 23-OCT-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..330  
US-08-957-001B-4

Query Match 68.4%; Score 270.8; DB 4; Length 330;  
Best Local Similarity 88.8%; Pred. No. 5.9e-78;  
Matches 293; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 61 gacattgtgtctacacagctccagattccctgtgctgtaagcttagagagagagcact 120  
DB 1 GACATTGTGTATATCAACAGTCTCCATCCACCTGGCTGTGTCAACAGAGAGAGGTCAC 60  
QY 121 attagctgcaaatccagctcagctgctgctcaacagtagaaccgagagaaactctgct 180  
DB 61 ATGAAGCTGCNAATCCAGTCCAGTGTCTGTTCAACAGTAGAACCAGAAAGAACTACTGGCT 120  
QY 181 tgggtcccaagcaaaacagagggcagcctcctaaactgtctatctactacgggcatccactagg 240  
DB 121 TGGTTCACAGCAAAACCAAGGAGCTCTCTAACTGCTATCTACTGCGCATCCACTAGG 180  
QY 241 gaattcgggtggtccctgtagcttcagctgagtgagtgatctgagagacagattcactccacc 300  
DB 181 GAATCTGGGGTCCCTGATGCTTCAACAGCAGTGCATCGGAGCATCTTCACTCTCACC 240  
QY 301 atcagcagctcgcagggctgaaagagctgagcagtttacttactgcaacgaattataact 360  
DB 241 ATCAGCAGAGTGTCTCAGGCTGAAGACCTGCGCATGTTATTACTGCAAGCAATCTATTATCT 300  
QY 361 tacacgttcgcagcagggagcacaagtgtgaa 390

DB 301 CGAGCGTTGCTGAGGACCAACAGCTTGAA 330  
RESULT 8  
US-09-496-301-4  
Sequence 4, Application US/09496301  
Patent No. 6248565  
GENERAL INFORMATION:  
APPLICANT: Williams, William V.  
APPLICANT: Madalo, Michael  
APPLICANT: Weiner, David B.  
TITLE OF INVENTION: IMPROVED VACCINES  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6248565ris  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/496,301  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/957,001  
FILING DATE: 23-OCT-1997  
APPLICATION NUMBER: US 60/029,592  
FILING DATE: 23-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: UPN-3303  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..330  
US-09-496-301-4

Query Match 68.4%; Score 270.8; DB 4; Length 330;  
Best Local Similarity 88.8%; Pred. No. 5.9e-78;  
Matches 293; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 61 gacattgtgtgacacagcttcacagattccctgtgctgtaagcttagagagagagcact 120  
DB 1 GACATTGTGTATATCAACAGTCTCCATCCACCTGGCTGTGTCAACAGAGAGAGGTCAC 60  
QY 121 attagctgcaaatccagctcagctgctgctcaacagtagaaccgagagaaactctgct 180  
DB 61 ATGAAGCTGCNAATCCAGTCCAGTGTCTGTTCAACAGTAGAACCAGAAAGAACTACTGGCT 120  
QY 181 tgggtcccaagcaaaacagagggcagcctcctaaactgtctatctacttactgcaacgaatt 240  
DB 121 TGGTTCACAGCAAAACCAAGGAGCTCTCTAACTGCTGATCTACTGCGCATCCACTAGG 180  
QY 241 gaattcgggtggtccctgtagcttcagctgagtgagtgatctgagagacagattcactccacc 300

|||||  
Db 181 GAATCTGGGGTCCCTGATCGCTTCACAGGCACTGGATCGGACAGATTCTCACTCCACC 240  
Qy 301 atcacagctctcagagctgaagagctgtgcaatttactgtacgcaatctataatct 360  
Db 241 ATCAGAGGTGCTGAGAGCTGAGACCTGTCGATTTACTGCAAGCAATCTTATATCTT 300  
Qy 361 tacacgtctcgacagggagcaaggctgga 390  
Db 301 CGGACGTCGTGGAGGCAACGACGCTGGA 330

## RESULT 9

US-09-423-439-47  
; Sequence 47, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423.439  
; FILING DATE: 09-NO. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 864 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
US-09-423-439-47

Query Match 68.3%; Score 270.6; DB 4; Length 864;

Best Local Similarity 86.0%; Pred. No. 1e-77; Mismatches 49; Indels 0; Gaps 0;

Matches 300; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 48 tggaccctgtgggacattgtgtcagacagctcagattccctgtgctgaagctagg 107  
Db 462 TGGCGGGGATCTGACATTGACCTCTCACAGTCTCCATCTCTCCCTGGCTGTGTACACAGG 521  
Qy 108 agagagggcaccattatgctgaatccagctcagagctgtcctcaacagtagaaccggaga 167  
Db 522 AAGAGAAGTCCACCATGAGTGCAGATCCAGTCCAGTCTCCCTCAACAGTAGAACCAGGANA 581  
Qy 168 gaactactgtgctgtgtacagcagaacacagggcagcctcctaaactgtgactactg 227  
Db 582 GAATCTACTTGCTGTGTACACAGAGACAGGAGGAGCTCTCTAAACTGCTGATCTATTG 641  
Qy 228 ggcattccactaaggaaatcggggctcctgctcagctcagtgcaagtgagatctggagcaga 287  
Db 642 GGCATCTACAGACATCTGGGGTCCCTGATCGCTTCACAGGACAGTAGATCTGGGACAGA 701

Qy 288 ttccactccaccatcagcagctcgcaggtcgaagagctgtgcaatttactgtacgca 347  
Db 702 TTTCACTCTACCATCAGCAGAGTGTGACGCTGAGAGCCTGCAATTTATCTGCAAGCA 761  
Qy 348 atctataatcttaccagcttgcagcagggagcgaagtggaataaana 396  
Db 762 ATCTTATCTCTCTGAGAGCTGTGGAGGACACCAAGCTCGAGATCAAA 810

## RESULT 10

US-09-423-439-31  
; Sequence 31, Application US/09423439  
; Patent No. 6339070  
; GENERAL INFORMATION:  
; APPLICANT: EMERY, Stephen Charles  
; BLAKEY, David Charles  
; TITLE OF INVENTION: CHEMICAL COMPOUNDS  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pillsbury Winthrop, L.L.P.  
; STREET: 1100 New York Ave., N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: MS Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/423.439  
; FILING DATE: 09-NO. 6339070-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB98/01294  
; FILING DATE: 05-MAY-1998  
; APPLICATION NUMBER: GB 9709421.3  
; FILING DATE: 10-MAY-1997  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2019 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-423-439-31

Query Match 68.3%; Score 270.6; DB 4; Length 2019;

Best Local Similarity 86.0%; Pred. No. 1.4e-77; Mismatches 49; Indels 0; Gaps 0;

Matches 300; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 48 tggaccctgtgggacattgtgtcagacagctcagattccctgtgctgaagctagg 107  
Db 453 TGGCGGGGATCTGACATTGAGCTCTCACAGTCTCCATCTCTCCCTGGCTGTGTACACAGG 512  
Qy 108 agagagggcaccattatgctgaatccagctcagagctgtcctcaacagtagaaccggaga 167  
Db 513 AAGAGAAGTCCACCATGAGTGCAGATCCAGTCCAGTCTCCCTCAACAGTAGAACCAGGANA 572  
Qy 168 gaactactgtgctgtgtacagcagaacacagggcagcctcctaaactgtgactactg 227  
Db 573 GAATCTACTTGCTGTGTACACAGAGACAGGAGCTCTCTAAACTGCTGATCTATTG 632  
Qy 228 ggcattccactaaggaaatcggggctcctgctcagctcagtgcaagtgagatctggagcaga 287  
Db 633 GGCATCTACAGACATCTGGGGTCCCTGATCGCTTCACAGGACAGTAGATCTGGGACAGA 692  
Qy 288 ttccactccaccatcagcagctcgcaggtcgaagagctgtgcaatttactgtacgca 347  
Db 693 TTTCACTCTACCATCAGCAGAGTGTGACGCTGAGAGCCTGCAATTTATCTGCAAGCA 752







Search completed: August 26, 2002, 16:15:01  
Job time: 4250 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 14:59:37 ; Search time 25.86 Seconds

(without alignments)  
490.479 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVILLILLMWSTGTCG.....YCTGSYNYTFSGGTKEIK 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	87.5	133	2 PS0023	Ig kappa chain pre
2	558.5	82.0	134	1 K4HU17	Ig kappa chain pre
3	558	81.9	120	2 G33932	Ig kappa chain pre
4	553.5	81.3	134	2 S49531	anti-Sm antibody V
5	552	81.1	133	1 K4HU1	Ig kappa chain pre
6	542.5	79.7	138	2 S26040	Ig kappa chain pre
7	541.5	79.5	145	2 PL0014	Ig kappa chain pre
8	539.5	79.2	134	2 PC1214	Ig kappa chain pre
9	536.5	78.8	135	2 S38807	Ig light chain V-J
10	536	78.7	138	2 A53261	Ig kappa chain pre
11	535.5	78.6	129	2 S40347	Ig kappa chain - h
12	532.5	78.2	240	2 S06084	Ig kappa chain pre
13	528.5	77.6	132	2 S46373	Ig kappa chain V-J
14	515.5	75.7	134	2 S21917	Ig kappa chain V r
15	515	75.6	121	1 K4HU	Ig kappa chain pre
16	510	74.9	113	2 PT0407	Ig light chain V r
17	506.5	74.4	120	2 S51147	antibody light cha
18	506.5	74.4	124	2 S40364	Ig kappa chain - h
19	506	74.3	112	2 S43103	Ig kappa chain V-J
20	502.5	73.8	113	2 S34002	Ig kappa chain V r
21	500.5	73.5	136	2 A49137	Ig kappa chain pre
22	497.5	73.1	114	1 K4HULN	Ig kappa chain V-I
23	494	72.5	112	2 PL0265	Ig kappa chain V r
24	493.5	72.5	129	2 S40329	Ig kappa chain V-J
25	492	72.2	113	2 PT0408	Ig light chain V r
26	490.5	72.0	113	2 S30520	Ig kappa chain V r
27	482	70.8	102	2 S41393	Ig kappa chain V r
28	480	70.5	113	2 PH1047	Ig light chain V r
29	476.5	70.0	113	2 S34003	Ig kappa chain V r

30	475	69.8	103	2 PH1052	Ig light chain V r
31	473.5	69.5	111	2 S03304	Ig kappa chain V r
32	473.5	69.5	114	2 S44116	Ig kappa chain V-J
33	473.5	69.5	114	2 S44119	Ig kappa chain V-J
34	471	69.2	104	2 PH1101	Ig light chain V r
35	470.5	69.1	113	2 S30523	Ig kappa chain V r
36	470	69.0	104	2 PH1102	Ig kappa chain V r
37	467	68.6	103	2 PH1051	Ig light chain V r
38	466	68.4	104	2 PH1050	Ig light chain V r
39	464	68.1	103	2 PH1050	Ig light chain V r
40	462.5	67.9	113	2 PL0263	Ig kappa chain V r
41	460	67.5	101	2 PH1046	Ig kappa chain V r
42	457	67.1	104	2 PH103	Ig light chain V r
43	452.5	66.4	113	2 PL0264	Ig light chain V r
44	452.5	66.4	214	2 S68212	Ig kappa chain (Ma
45	452	66.4	106	2 A49138	IgA kappa rheumato

## ALIGNMENTS

## RESULT 1

PS0023

Ig kappa chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence, revision 07-Jun-1990 #text\_change 21-Jan-2000

C:Accession: PS0023

R:Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dorney, H.

Gene 74: 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains

A:Reference number: PS0023; MUID:89232725

A:Accession: PS0023

A:Molecule type: mRNA

A:Residues: 1-133 <MAR>

A:Experimental source: strain BALB/c

A>Note: the amino-terminal four residues of the mature protein were directly sequence

C:Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aer

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>

F:36-116/Domain: immunoglobulin homology <IMV>

Query Match Best Local Similarity 87.5%; Score 596; DB 2; Length 133;

Matches 114; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Oy 1 MDSQAQVILLILLMWSTGCDIVLTQSPDSLAVSIGERATISCKSSQSLNSRTRENTLA 60

Db 1 MDSQAQVILLILLMWSTGCDIVMSQSPSLAVSAGEKVTMSCKSSQSLNSITRKNFLA 60

Oy 61 WYQKPGQPKLLTYWASTRESGVDPRTGSGSGGDFLTSSLOAEVAYVYCCQSNL 120

Db 61 WYQKPGQPKLLTYWASTRESGVDPRTGSGSGGDFLTSSLOAEVAYVYCCQSNL 120

Oy 121 YTFGGTKEIK 132

Db 121 RTFGGTKEIK 132

## RESULT 2

K4HU17

Ig kappa chain precursor V-IV region (B17) - human

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence, revision 30-Jun-1987 #text\_change 21-Jan-2000

C:Accession: A01905

R:Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A:Title: Detection of a unique human V kappa parv germline gene by a cloned cDNA probe.

A:Reference number: A01905; MUID:86041854

A:Accession: A01905

A:Molecule type: mRNA





[illegible]

```

A:Residues: 1-145 <CHB>
C:Experimental source: cell line F6-3
C:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphoryl
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-134/Product: Ig heavy chain V region (C11) #status predicted <Mat>
F:36-116/Domain: immunoglobulin homology <IMM>
F:44-60/Region: complementarity-determining 1
F:76-82/Region: complementarity-determining 2
F:115-123/Region: complementarity-determining 3
F:135-145/Domain: constant region (fragment) #status predicted <COR>

Query Match 79.5%; Score 541.5; DB: 2; Length 145;
Best Local Similarity 77.6%; Pred. No. 5.7e-39;
Matches 104; Conservative 18; Mismatches 9; Indels 3; Gaps 2;

OY 1 MDSQAQVILLILLMWSTGCGDIVLTQSPDSLAVSGERATISCKSSQSLNSRTRENYLA 60
DB 1 MDSQAQVILLILLMWSTGCGDIVMSQSPSLAVSGEKVMTSCQSSQSLVLTNSNQKNFLA 60

OY 61 WYQAKPGCPKLLIYMASTRSGVDPDRFSGSGSGTDFLTITSSLAQEDVAVYYCTQSYNL 120
DB 61 WYQAKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITSSVKAEDLAVYYC-QQYDS 119

OY 121 Y--TFGGGTKEIK 132
DB 120 YLTFGGGTKEIK 133

RESULT 8
PC1214
Ig kappa chain precursor V region (mab H8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PC1214
R:Hong, H.U.; Kim, A.K.; Ryu, C.J.; Park, S.S.; Chung, H.K.; Kwon, K.S.; Kim, K.L.; K
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A:Reference number: PC1213; MUID:93077049
A:Accession: PC1214
A:Molecule type: mRNA
A:Residues: 1-134 <HON>
A:Cross-references: GB:M98042; NID:g196749; PIDN:AAA38777.1; PID:g196750
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-134/Product: Ig light chain V region #status predicted <Mat>
F:36-116/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 539.5; DB: 2; Length 134;
Best Local Similarity 78.9%; Pred. No. 7.7e-39;
Matches 105; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 1 MDSQAQVILLILLMWSTGCGDIVLTQSPDSLAVSGERATISCKSSQSLNSRTRENYLA 60
DB 1 MDSQAQVILLILLMWSTGCGDIVMSQSPSLAVSGEKVMTSCQSSQSLVLTNSIQKNLA 60

OY 61 WYQAKPGCPKLLIYMASTRSGVDPDRFSGSGSGTDFLTITSSLAQEDVAVYYCTQSYNL 120
DB 61 WYQAKPGSPKLLIYMASTRSGVDPDRFTGSGSGTDFLTITSSNKAEDLAVYYCQQYYNY 120

OY 121 -YTFGGGTKEIK 132
DB 121 PSTFGGTKEIK 133

RESULT 9
S38807
Ig light chain V-J region - mouse
C:Species: Mus musculus (house mouse)

```







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:05:39 ; Search time 15.59 Seconds

(without alignments)  
327,837 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 1 MDSQAQVILLILLMWSTGCG.....YCTGSYNLTYTGCGTKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571.5	83.9	134	1	KV4C_HUMAN
2	552	81.1	133	1	KV4B_HUMAN
3	515	75.6	121	1	KV4A_HUMAN
4	502.5	73.8	114	1	KV4A_HUMAN
5	446	65.5	129	1	KV3H_HUMAN
6	442	64.9	129	1	KV3L_HUMAN
7	440	64.6	129	1	KV3M_HUMAN
8	418	61.4	133	1	KV2E_HUMAN
9	416.5	61.2	129	1	KV1I_HUMAN
10	409.5	60.1	128	1	KV3K_HUMAN
11	408.5	60.0	131	1	KV3I_MOUSE
12	408.5	60.0	132	1	KV3F_MOUSE
13	396	58.1	115	1	KV3I_HUMAN
14	394.5	57.9	116	1	KV3J_HUMAN
15	394	57.9	110	1	KV3P_MOUSE
16	393.5	57.8	136	1	KV5B_MOUSE
17	392.5	57.6	149	1	KV5A_MOUSE
18	384	56.4	109	1	KV3B_HUMAN
19	384	56.4	109	1	KV3F_HUMAN
20	383	56.2	111	1	KV3D_HUMAN
21	382.5	56.2	111	1	KV3M_MOUSE
22	382.5	56.2	111	1	KV3O_MOUSE
23	381	55.9	109	1	KV3E_HUMAN
24	380.5	55.9	117	1	KV1M_HUMAN
25	380.5	55.9	108	1	KV1M_HUMAN
26	380.5	55.9	111	1	KV3J_MOUSE
27	379.5	55.7	111	1	KV3U_MOUSE
28	377.5	55.4	111	1	KV3H_MOUSE
29	375.5	55.1	111	1	KV3N_MOUSE
30	374.5	55.0	111	1	KV3O_MOUSE
31	374.5	55.0	111	1	KV3R_MOUSE
32	374.5	55.0	111	1	KV3S_MOUSE
33	373.5	54.8	115	1	KV2A_HUMAN

34	370	54.3	109	1	KV3G_HUMAN	P04206	homo sapien
35	368.5	54.1	117	1	KV1J_HUMAN	P01602	homo sapien
36	368.5	54.1	129	1	KV1X_HUMAN	P04432	homo sapien
37	367	53.9	108	1	KV3A_HUMAN	P01619	homo sapien
38	366.5	53.8	108	1	KV1V_HUMAN	P04430	homo sapien
39	366.5	53.8	111	1	KV3D_MOUSE	P03977	mus musculus
40	366.5	53.8	111	1	KV3J_MOUSE	P01662	mus musculus
41	366.5	53.8	111	1	KV3T_MOUSE	P01672	mus musculus
42	366.5	53.8	114	1	KV1A_MOUSE	P01632	mus musculus
43	365.5	53.7	108	1	KV1H_HUMAN	P01600	homo sapien
44	362.5	53.2	111	1	KV3C_MOUSE	P01656	mus musculus
45	362	53.2	113	1	KV2B_HUMAN	P01615	homo sapien

## ALIGNMENTS

RESULT 1	KV4C_HUMAN	STANDARD:	PRT: 134 AA.
ID	KV4C_HUMAN		
AC	P06314;		
DT	01-JAN-1988 (Rel. 06, Created)		
DT	01-APR-1988 (Rel. 07, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Ig kappa chain V-IV region B17 precursor.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-86041854; PubMed-2997713;		
RA	Marsh P., Mills F., Gould H.;		
RT	"Detection of a unique human V kappa IV germline gene by a cloned		
RT	cDNA probe.";		
RL	Nucleic Acids Res. 13:6531-6544(1985).		
RP	REVISION TO 76.		
RA	Marsh P.;		
RL	Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.		
CC	-----		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
CC	EMBL; X02990; CA26733.1; -.		
DR	PIR; A01905; KAHU17.		
DR	HSSP; P01789; IMCP.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IgV; 1.		
FW	Immunoglobulin V region: Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	134
FT	DOMAIN	21	43
FT	DOMAIN	44	60
FT	DOMAIN	61	75
FT	DOMAIN	76	82
FT	DOMAIN	83	114
FT	DOMAIN	115	121
FT	DOMAIN	122	133
FT	DISUFID	43	114
FT	NON_TER	134	134
SEQ	SEQUENCE	134 AA;	14966 MW; 6413A22PD0738832 CRC64;

Query Match 83.9%; Score 571.5; DB 1; Length 134;  
Best Local Similarity 86.2%; Pred. No. 2e-52;

Matches	112:	Conservative	6:	Mismatches	11:	Indels	1:	Gaps	1:
QY	4	CAQVLLILLWVSGTCGDIVLTQSPDSLAVSLGERATITCKSSQSLNSRRENTLAWYQ	63						
Db	4	QROVSLTLWLTWISGAYGVDMQSPDSLAVSLGERATITCKSSQSLNSRRENTLAWYQ	63						
QY	64	OKPGCPKLLIYMASTRBSGVPDRFSSGSGSGTDFLTITSSLOAEVAVYYCCQSYNL-YT	122						
Db	64	OKPGCPKLLIYMASTRBSGVPDRFSSGSGSGTDFLTITSSLOAEVAVYYCCQSYNL-PT	123						
QY	123	FGQGTGKVEIK	132						
Db	124	FGQGTGKVEIK	133						
RESULT 2									
KY4B_HUMAN		STANDARD:		PRT:		133 AA.			
AC	P06313;								
DT	01-JAN-1988 (Rel. 06, Created)								
DT	01-JAN-1988 (Rel. 06, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	15-kappa chain v-IV region J1 precursor.								
OS	Homo sapiens (Human).								
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=66041853; PubMed=2997712;								
RA	Klobeck H.G., Bornkamm G.W., Combario G., Mocikat R., Pohlenz H.D.,								
RA	Zachau H.G.;								
RT	"Subgroup IV of human immunoglobulin K light chains is encoded by a								
RT	single germline gene.";								
RL	Nucleic Acids Res. 13:6515-6529(1985).								
CC	-----								
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).								
CC	-----								
DR	EMBL; Z00022; CAAT7317.1; -								
DR	PIR; A01904; K4HUT.								
DR	HSSP; P01789; IMCP.								
DR	InterPro; IPR003006; IG_MHC.								
DR	InterPro; IPR003596; IG_V.								
DR	Pfam; PF00047; Ig; 1.								
DR	SMART; SM00406; IGV; 1.								
KW	Immunoglobulin V region; Signal.								
FT	SIGNAL	1	20						
FT	CHAIN	21	133						
FT	DOMAIN	1	43						
FT	DOMAIN	21	44						
FT	DOMAIN	44	60						
FT	DOMAIN	61	75						
FT	DOMAIN	76	82						
FT	DOMAIN	83	114						
FT	DOMAIN	115	122						
FT	DOMAIN	123	132						
FT	DISULFID	43	114						
FT	NON_TER	133	133						
SQ	SEQUENCE	133 AA;	14632 MM;	5FB3953066744AF4	CNC64;				
Query Match									
Best Local Similarity		81.1%;		Score 552;		DB 1;		Length 133;	
Matches		108;		Conservative		6;		Mismatches 15;	

QY	64	QKPGPRLKLLIYMASTRRESGVDPDRSGSGSGTDFTLTITSSQLAQEDVAVYYCTQSNLYTF	123
DB	64	QKPGPRLKLLIYMASTRRESGVDPDRSGSGSGTDFTLTITSSQLAQEDVAVYYCQYDTPTPF	123
OY	124	GGGTVEIK 132	
DB	124	GGGTVEIK 132	
		RESULT 3	
		KV40_HUMAN	
AC	P06312	STANDARD:	PTT: 121 AA.
DT	01-JAN-1988	(Rel. 06, Created)	
DT	01-JAN-1988	(Rel. 06, Last sequence update)	
DT	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	IG kappa chain V-IV region precursor (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OK	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=86041853; PubMed=29971712;		
RA	Klobeck H.G., Bornkamm G.W., Combrlatto G., Mocikat R., Pohlenz H.D.,		
RA	Zachau H.G.;		
RT	"Subgroup IV of human immunoglobulin k light chains is encoded by a		
RL	single germline gene."		
CC	Nucleic Acids Res 13:6515-6529(1985).		
CC	-1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.		
CC	-----		
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL; 200023; CAAT7318.1; -.		
DR	PIR; A01902; K4H0;		
DR	HSSP; P01789; IMCP.		
DR	Interpro; IPR003006; IG_MHC.		
DR	Interpro; IPR003596; IG_V.		
DR	Pfam; PF00047; Ig_1.1.		
DR	SMART; SM00406; IGV; 1.		
KM	Immunoglobulin V region; Signal.		
FT	SIGNAL	1	20
FT	CHAIN	21	>121
FT	DOMAIN	21	43
FT	DOMAIN	44	60
FT	DOMAIN	61	75
FT	DOMAIN	76	82
FT	DOMAIN	83	114
FT	DOMAIN	115	121
FT	DISULFID	43	114
FT	NON_TER	121	121
SO	SEQUENCE	121 AA;	13380 MW; 9586AD418BD33974 CRC64;
	Query Match	75.6%;	Score 515; DB 1; Length 121;
	Best Local Similarity	85.3%;	Pred. No. 1.3e-46;
	Matches	99; Conservative	6; Mismatches 11; Indels 0; Gaps 0;
OY	4	QAQVILLILLWVSGGCDIVLTQSPDSLAVSLGERATITSCASSQSGLNSRPRTANTAYQ	63
DB	4	QGVQVILLIWMVSGGYIVMTQSPDSLAVSLGERATITCKSSQSVLYSSNNKNTLAYQ	63
OY	64	QKPGPRLKLLIYMASTRRESGVDPDRSGSGSGTDFTLTITSSQLAQEDVAVYYCTQSN 119	
DB	64	QKPGPRLKLLIYMASTRRESGVDPDRSGSGSGTDFTLTITSSQLAQEDVAVYYCQYIS 119	

```

RESULT 4
KV3L_HUMAN STANDARD; PRT; 114 AA.
ID KV3L_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
RT subgroup IV of the kappa type (Bence-Jones protein Len).";
RL Hope-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN [2]
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (Aug-1996) to the SWISS-PROT data bank
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP; P01789; 1MCP.
DR DOMAIN 44 54 FRAMEWORK-2.
FT DOMAIN 55 69 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 FRAMEWORK-3.
FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 129 129 K1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match
Best Local Similarity 73.8%; Score 502.5; DB 1; Length 114;
Matches 98; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

OY 21 DIVLTQSPDSLAIVSGERATISCKSSQSLNSTRRENYLAIVQKFGQPKLLIYNASTR 80
DB 1 DIVLTQSPDSLAIVSGERATISCKSSQSLNSTRRENYLAIVQKFGQPKLLIYNASTR 60
OY 81 ESGVDFRFGSGSGDTFTLTISLQAEADVAVVYCTQSYNLTFFEGGTQVEIK 132
DB 61 ESGVDFRFGSGSGDTFTLTISLQAEADVAVVYCTQSYNLTFFEGGTQVEIK 113

RESULT 5
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;

```

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RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Cird J.G., Chen P.P.,
RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC -----
DR EMBL; M12740; AA58992.1; -
DR PIR; A01898; K3HUCI.
DR HSSP; P01789; 1MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 FRAMEWORK-3.
FT DOMAIN 119 129 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 129 129 K1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64;

Query Match
Best Local Similarity 65.5%; Score 446; DB 1; Length 129;
Matches 90; Conservative 20; Mismatches 15; Indels 10; Gaps 3;

OY 1 MDSQAVLILLILLVSGTGDIVLTQSPDSLAIVSGERATISCKSSQSLNSTRRENYLA 60
DB 1 MEAPQGLIFLLILMLPPTTGELVWTQSPATILSYSPGERATISCAASQSVSN-----LA 54
OY 61 WYQKPGQPKLLIYMASTRGSGVDFRFGSGSGDTFTLTISLQAEADVAVVYCTQSYN- 119
DB 55 WYQKPGQPKLLIYMASTRGSGVDFRFGSGSGDTFTLTISLQAEADVAVVYCTQSYN 113
OY 120 --LYTFGGTQVEIK 132
DB 114 WPPWTFGGGTQVEIK 128

RESULT 6
KV3L_HUMAN STANDARD; PRT; 129 AA.
ID KV3L_HUMAN
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).

```

-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCLYTIC LEUKEMIA.

CC PIR: PLO022; K3HUA.  
 DR HSSP: P01789; 1MCP.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR Immunoglobulin V region; signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129  
 FT DOMAIN 21 43  
 FT DOMAIN 44 55  
 FT DOMAIN 56 70  
 FT DOMAIN 71 77  
 FT DOMAIN 78 109  
 FT DOMAIN 110 118  
 FT DOMAIN 119 129  
 FT DISULFID 43 109  
 FT NON\_TER 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3G55292772774D0 CRC64;

Query Match 64.9%; Score 442; DB 1; Length 129;  
 Best Local Similarity 66.9%; Pred. No. 5.2e-39;  
 Matches 89; Conservative 19; Mismatches 19; Indels 6; Gaps 2;

QY 1 MDSQAVLILLWVSGTGVILVTPSPSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 1 METPAQLLLLLMLPDTTGEIVLTOSPGTSLSPGERATLSRAASQVSSS-----YLA 55  
 DB 61 WYQKPGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLQAEVAVYCTQ-SYN 119  
 119  
 DB 56 WYQKPGQAPRLIYGAASSNATGIPDRFGSGSGTDFTLTISLPEDPFAVYCCQYGS 115  
 QY 120 LYTFGGCTKVEIK 132  
 DB 116 PRTFGGCTKVEIK 128

RESULT 7  
 KV3M\_HUMAN STANDARD; PRT; 129 AA.  
 ID KV3M\_HUMAN  
 AC P18136;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE 15 Kappa chain V-III region HIC precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88171307; PubMed=3127527;  
 RA Klips T.J., Tomhave E., Chen P.P., Carson D.A.;  
 RT "Autoantibody-associated kappa light chain variable region gene  
 RT expressed in chronic lymphocytic leukemia with little or no somatic  
 RT mutation. Implications for etiology and immunotherapy.";  
 J. Exp. Med. 167:840-852(1988).  
 -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCLYTIC  
 CC LEUKEMIA.  
 DR PIR: PLO022; K3HUA.  
 DR HSSP: P01789; 1MCP.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR Immunoglobulin V region; signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.

FT DOMAIN 21 43  
 FT DOMAIN 44 55  
 FT DOMAIN 56 70  
 FT DOMAIN 71 77  
 FT DOMAIN 78 109  
 FT DOMAIN 110 118  
 FT DOMAIN 119 129  
 FT DISULFID 43 109  
 FT NON\_TER 129  
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EAB2B74D6 CRC64;

Query Match 64.6%; Score 440; DB 1; Length 129;  
 Best Local Similarity 66.2%; Pred. No. 8.4e-39;  
 Matches 88; Conservative 20; Mismatches 19; Indels 6; Gaps 2;

QY 1 MDSQAVLILLWVSGTGVILVTPSPSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 1 METPAQLLLLLMLPDTTGEIVLTOSPGTSLSPGERATLSRAASQVSSS-----YLA 55  
 DB 61 WYQKPGQPKLLIYWASTRESGVDPDRFGSGSGTDFTLTISLQAEVAVYCTQ-SYN 119  
 119  
 DB 56 WYQKPGQAPRLIYGAASSNATGIPDRFGSGSGTDFTLTISLPEDPFAVYCCQYGS 115  
 QY 120 LYTFGGCTKVEIK 132  
 DB 116 PRTFGGCTKVEIK 128

RESULT 8  
 KV2E\_HUMAN STANDARD; PRT; 133 AA.  
 ID KV2E\_HUMAN  
 AC P06310;  
 DT 01-JAN-1988 (Rel. 106, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 138, Last annotation update)  
 DE 15 Kappa chain V-II region RPMI 6410 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041852; PubMed=2997711;  
 RA Klobbeck H.G., Melndl A., Combrilato G., Solomon A., Zachau H.G.;  
 RT "Human immunoglobulin kappa light chain genes of subgroups II and  
 RT III.";  
 RL Nucleic Acids Res. 13:6499-6513(1985).  
 CC -----  
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 CC -----  
 CC EMBL: 200020; CAA77315.1; -  
 DR PIR: A01890; K2HURP.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; 1g; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR Immunoglobulin V region; signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 133  
 FT DOMAIN 21 43  
 FT DOMAIN 44 59  
 FT DOMAIN 60 74  
 FT DOMAIN 75 81  
 FT DOMAIN 82 113  
 FT DOMAIN 114 122  
 FT DOMAIN 123 132 IG KAPPA CHAIN V-II REGION RPMI 6410.  
 FRAMEWORK-1.  
 FRAMEWORK-2.  
 FRAMEWORK-3.  
 FRAMEWORK-4.





Oy	51	MYQOKPQGPPILLIYMASTRSGVPDPRFSSGSDTDTLTSSLOADVVAVCTO-syn	119
		: : : : :           :           :	
Dd	55	MYQOKRGSPALLLRDMSSRANGIPDFNFSGSSTDPITLIRLEPDFAVNYCCQYSTS	114
Oy	120	LYTFGGGTAKVEIK	132
		: : : : :	
Dd	115	PYTFGGATKLEIK	127

	RESULT	11
KVJL_MOUSE		
ID	KVJL_MOUSE	STANDARD; PRT; 131 AA.
AC	P01661;	
DT	21-JUL-1986 (Rel. 01, Created)	
DR	21-JUL-1986 (Rel. 01, Last sequence update)	
DY	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig kappa chain V-II region MOPC 63 precursor.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE OF 1-35.	
RX	MEDLINE=7823587; Pubmed=98179;	
RA	Burstein Y., Schechter I.;	
RT	"Primary structures of N-terminal extra peptide segments linked to	
RT	the variable and constant regions of immunoglobulin light chain	
RT	precursors: implications on the organization and controlled	
RT	expression of immunoglobulin genes."	
RL	Biochemistry 17:2392-2400(1978).	
RN	[2]	
RP	SEQUENCE OF 21-131.	
RX	MEDLINE=73140225; Pubmed=4691517;	
RA	McKean D.J., Potter M., Hood L.E.;	
RT	"Mouse immunoglobulin chains. Pattern of sequence variation among	
RT	kappa chains with limited sequence differences."	
RL	Biochemistry 12:760-771(1973).	
RN	[3]	
RP	REVISIONS.	
RX	MEDLINE=79012520; Pubmed=99744;	
RA	McKean D.J., Bell M., Potter M.;	
RT	"Mechanisms of antibody diversity: multiple genes encode structurally	
RT	related mouse kappa variable regions."	
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).	
DR	PIR: A01935; KVM5M6.	
DR	HSSP: P01789; IMCP.	
DR	InterPro: IPRO03006; Ig_MHC.	
DR	InterPro: IPRO03596; Ig_v.	
DR	PIfam: PF00047; Ig; 1.	
DR	SMART: SMO0406; IGv; 1.	
KW	Immunoglobulin V region; Signal.	
FT	SIGNAL	1 20
FT	CHAIN	21 131
FT	DOMAIN	21 43
FT	DOMAIN	44 58
FT	DOMAIN	59 73
FT	DOMAIN	74 80
FT	DOMAIN	81 112
FT	DOMAIN	113 121
FT	DOMAIN	122 131
FT	DISULFID	43 112
FT	NON TER	131 131
SO	SEQUENCE	131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match	60.0%; Score 408.5; DB 1; Length 131;	
Best Local Similarity	62.4%; Pred. No. 1,6e-35;	
Matches	83; Conservative 21; Mismatches 26; Indels 3; Gaps	
DB	1 MSDAAQVLITLLLVSGTGDIVTQSPPDSLAVSLGERTATSCSKSSOLNSLTRENYLA 60	
db	1 METPTLLLVLLVLPVGSTGNIVLTQSPASISLALGORARTISCASSV--DSYGNSFMH 58	

Qy	61	WYQOKPGPPELLLYMSTRSGVDPDRFFSGSGSTDTLLTISLQADVAVYCTQ	-syn	119
Db	59	WYQOKPGPPELLLYLMSNLDSGVDPARFSSGSGSTDTLLTIDPEADNADATYYCCQNNED		118
Qy	120	LYTFGGGTAKVEIK		132
Db	119	PWTFGGGTKEIK		131

[illegible]

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Db      59 *WZZKRGAPGPKLLIYRASNLSCIPARRSGSGSRIBFLTLTIBPVABDVAYVFCZ2S2B 118
Oy      120 LYTSGGTKEIK 132
Db      119 PWTFGSGTKLEIK 131

RESULT 13
KV31_HUMAN STANDARD; PRT; 115 AA.
AC      P04433;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region V6 precursor (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxId:9606;
[1]
SEQUENCE FROM N.A.
RX      MEDLINE=85087932; PubMed=6440122;
RA      Pech M., Zachau H.G.;
RT      "Immunoglobulin genes of different subgroups are interdigitated
RL      within the VK locus."
RL      Nucleic Acids Res. 12:9229-9236(1984).
CC      -----
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CC      -----
DR      EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR      PIR; A01900; K3HDVG.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IgV; 1.
DR      KIMM; KIMM0001; V region; Signal.
FT      SIGNAL          1      20
FT      CHAIN           21     >115
FT      DOMAIN          21     43      IG KAPPA CHAIN V-II REGION VG.
FT      DOMAIN          44     54      FRAMEWORK-1.
FT      DOMAIN          55     69      COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN          70     76      FRAMEWORK-2.
FT      DOMAIN          77     108     COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN          109    115     FRAMEWORK-3.
FT      DISULFID        43     108     COMPLEMENTARITY-DETERMINING-3.
FT      NON_TER         115
SO      SEQUENCE        115 AA; 12575 MM; 2DE47CDA3A17D555 CXC64;

Query Match      58.1%; Score 396; DB 1; Length 115;
Best Local Similarity 65.5%; Pred. No. 2,7e-34;
Matches 78; Conservative 17; Mismatches 18; Indels 6; Gaps 1;

Oy      1 MDSQAQVILLILLVWSTGCGDIVLTQSPDSLAVSLGERATISCKSSQSLNSTRNTYLA 60
Db      1 MEAPQAQLLELLMLPDTTGEIVLTQSPATLSLSPGERATISCRASQSV-----SYLA 54
Oy      61 WYQKPGQPKLLIYMASTRSGVDRRSQSGSGDFLTITSSLDQAEVAYVYCTQSTN 119
Db      55 WYQKPGQPKLLIYDASNRATGIPARRSGSGSGDFLTITSSLEPEDFAVYVYCCOQRN 113

RESULT 14
KV31_HUMAN STANDARD; PRT; 116 AA.
ID      KV31_HUMAN
AC      P04434;

```

DT	13-AUG-1987 (Rel. 05, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-III region VH precursor (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OK	NCBI_TaxID=9606;
RN	(1)
RP	SEQUENCE FROM N.A.
RX	MEDLINE=85087932; PubMed=6440122;
RA	Pech M., Zachau H.G.;
RT	"Immunoglobulin genes of different subgroups are interdigitated
RL	within the VK locus.";
CC	Nucleic Acids Res. 12:9229-9236(1984).
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; X02725; -- NOT_ANNOTATED_CDS.
DR	PIR; A01901; K3HOVH.
DR	HSSP; P01789; 2MCP.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
KW	Immunoglobulin V region; Signal.
FT	CHAIN 1 20
FT	SIGNAL 1 20
FT	DOMAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT	DOMAIN 21 43 FRAMEWORK-1.
FT	DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 56 70 FRAMEWORK-2.
FT	DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 78 109 FRAMEWORK-3.
FT	DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT	DISULFID 43 109 BY SIMILARITY.
FT	NON TER 116 116
SO	SEQUENCE 116 AA; 12757 MW; 51CDS5BA53B21929 CRC64;
QY	Query Match 57.9%; Score 394.5; DB 1; Length 116;
	Best Local Similarity 64.2%; Pred. No. 3.9e-34;
	Matches 77; Conservative 18; Mismatches 20; Indels 5; Gaps 1;
QY	1 MDSQAOVLILLLLWVSGTGDIVLTPSDSLAVSLGERATISCKSSQSLNSRRENYLA 60
DB	1 MEAPQAQLLELLMLPDPTRREIVMGSPTLSLSPGERVTLSCRASQSVSSS----YLT 55
OY	61 WYQAKPGCPKRLIYASTRESGVDRNRSGSGSGTDFLLTISLQAEVAVNYTCQTSLN 120
DB	56 WYQAKPGCAPRLIYGASTRATSIPIARFSGSGSGTDFLLTISLQAEVAVNYTCQDHN 115
RESULT	15
KV3P_MOUSE	STANDARD; PRT; 110 AA.
AC	P01686;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-III region PC 7210.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK	NCBI_TaxID=10090;
RN	(1)
RP	SEQUENCE.
RX	MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gattalman L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 RT diversity";  
 RT Nature 276:785-790(1978).  
 RU PIR: D01937; KWS10.  
 DR HSSP: P01789; IMCP.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_V.  
 DR Pfam: PF00047; Ig: 1.  
 DR SMART: SM00406; IGV: 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 100  
 FT DOMAIN 101 110  
 FT DISULFID 23 92  
 FT NON\_TER 110  
 SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;  
 FRAMEWORK-1.  
 COMPLEMENTARITY-DETERMINING-1.  
 FRAMEWORK-2.  
 COMPLEMENTARITY-DETERMINING-2.  
 FRAMEWORK-3.  
 COMPLEMENTARITY-DETERMINING-3.  
 FRAMEWORK-4.  
 BY SIMILARITY.

Query Match 57.9%; Score 394; DB 1; Length 110;  
 Best Local Similarity 70.5%; Pred. No. 4, 1e-34;  
 Matches 79; Conservative 11; Mismatches 20; Indels 2; Gaps 1;  
 OY 21 DIVLTQSPDLSAVSLGERATISCKSSQSLNSRTRENTLAWYQKPGOPKLLITYASTR 80  
 DB 1 DIVLTQSPDLSAVSLGQRATISCKASQSL--DYGDSTNMWYQKPGOPKLLITYASNL 58  
 OY 81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCTOSYNLYTGGGTKEIK 132  
 DB 59 ESGIPARFSGSGSGTDFTLTINHPVEEDATYCYCHQSEDPMTFGSGTKLEIK 110

Search completed: August 26, 2002, 15:05:39  
 Job time: 358 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 26, 2002, 15:05:03 ; Search time 36.13 Seconds

(without alignments)  
632.032 Million cell updates/sec

Title: us-09-249-011-8

Perfect score: 681  
Sequence: 1 MDSQAQYLILLLMWSTGCG.....YCTOSYNLYFGGQTKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : SPTREMBL.19.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	410.5	60.3	107	11 Q9ER29	Q9ER29 mus musculu
2	400	58.7	238	11 Q99M37	Q99M37 mus musculu
3	388	57.0	107	4 Q96SA9	Q96SA9 homo sapien
4	384	56.4	107	4 Q9UL81	Q9UL81 homo sapien
5	383.5	55.3	111	11 Q920E9	Q920E9 mus musculu
6	379.5	55.7	108	4 Q9UL77	Q9UL77 homo sapien
7	379	55.1	109	4 Q9UL78	Q9UL78 homo sapien
8	375.5	54.8	108	4 Q9UL79	Q9UL79 homo sapien
9	373.5	54.7	108	4 Q9UL83	Q9UL83 homo sapien
10	372.5	54.0	109	4 Q9UL86	Q9UL86 homo sapien
11	368	54.0	109	4 Q9UL85	Q9UL85 homo sapien
12	352.5	51.8	114	4 Q9UL80	Q9UL80 homo sapien
14	348.5	51.2	234	11 Q91WF8	Q91WF8 mus musculu
15	341	50.1	104	11 Q91L82	Q91L82 mus musculu
16	339.5	49.9	233	11 Q91WS9	Q91WS9 mus musculu

17	336.5	49.4	99	11 Q91L74	Q91L74 mus musculu
18	331.5	48.7	214	11 Q91L85	Q91L85 mus musculu
19	324.5	47.7	103	11 Q91L80	Q91L80 mus musculu
20	319.5	46.9	116	4 Q96PE6	Q96PE6 homo sapien
21	319	46.8	130	4 Q9NP29	Q9NP29 homo sapien
22	315.5	46.3	298	11 Q9QXF0	Q9QXF0 mus musculu
23	315	46.3	235	11 Q91W12	Q91W12 mus musculu
24	308.5	45.3	109	11 Q920E6	Q920E6 mus musculu
25	307.5	45.2	127	11 Q925S9	Q925S9 mus musculu
26	303.5	44.6	101	11 Q91L78	Q91L78 mus musculu
27	303.5	44.6	109	6 Q9N0W5	Q9N0W5 oryctolagus
28	300	44.1	241	11 Q921A6	Q921A6 mus musculu
29	296.5	43.5	107	11 Q91L84	Q91L84 mus musculu
30	292	42.9	106	5 Q9U410	Q9U410 schistosoma
31	286.5	42.1	211	11 Q91XL0	Q91XL0 mus musculu
32	280.5	41.2	97	11 Q91L76	Q91L76 mus musculu
33	257.5	37.8	218	11 Q925S1	Q925S1 mus musculu
34	243	35.7	107	4 Q9NSD6	Q9NSD6 homo sapien
35	242.5	35.6	236	4 Q96E61	Q96E61 homo sapien
36	240.5	35.3	108	4 Q96S80	Q96S80 homo sapien
37	238	34.9	235	11 Q99M11	Q99M11 mus musculu
38	233.5	34.3	107	4 Q9UL82	Q9UL82 homo sapien
39	226.5	33.3	112	4 Q96JD1	Q96JD1 homo sapien
40	217	31.9	116	4 Q96JD0	Q96JD0 homo sapien
41	215	31.6	112	4 Q96JD2	Q96JD2 homo sapien
42	207	30.4	233	11 Q91V32	Q91V32 m adult mal
43	192.5	28.3	233	4 Q96I69	Q96I69 homo sapien
44	191	28.0	109	11 Q9ET13	Q9ET13 mus musculu
45	178	26.1	154	11 Q91XK2	Q91XK2 mus musculu

## ALIGNMENTS

RESULT 1  
Q9ER29 ID Q9ER29 PRELIMINARY; PRT; 107 AA.  
AC Q9ER29;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;  
RT "Cloning and sequencing of the light chain fragment of variable region  
RT genes of an anti-hTNF-a monoclonal antibody.";  
RL J. Cell. Mol. Immunol. 12:21-26(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RT "Construction and sequencing of the single-chain antibody gene of a  
RT human TNF-alpha specific monoclonal antibody.";  
RL T1 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF62753; AAG23804.1; -  
DR HSSP: P80362; 1WTL.  
DR InterPro: IPR003599; I9.  
DR InterPro: IPR003006; I9.  
DR InterPro: IPR003596; I9LV.  
DR Pfam: PF00047; I9; 1.  
DR SMART: SM00409; I9; 1.  
DR SMART: SM00406; I9V; 1.  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11784 MW; 2B15DEA6604A26C3 CRC64;



Oy	81	ESGVDRRSGSGSCTDFTLTITSSLOAEDVAVYYCQSNLNTFYGGGTVEIK	132
Dd	55	QSGVSRSGSGSGTDFTLTISGLAEDFAVFATYCCOOSYSALEFFGPGTKVDIR	106
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RESULT	5		
ID	0920E9	PRELIMINARY;	PRT; 111 AA.
AC	0920E9;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DE	PTERIN-MICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Atkin J.D., Tape A., Jennings I.G., Horatis O., Cotton R.G.H.;		
RT	"Definition of the Idiotope of Pterin-Micking Antibodies Expressed in Mammalian Cells."		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
EMBL	AF307935; AAL09419.1; -.		
FT	NON_TER	1	
FT	NON_TER	111	
SQ	SEQUENCE	111 AA; 12046 MW; IE46988AA6858526 CRC64;	
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Query Match 56.3%; Score 383.5; DB 11; Length 111; Best Local Similarity 69.9%; Pred. No. 2.7e-33; Matches 79; Conservative 11; Mismatches 20; Indels 3; Gaps 2;			
Oy	21	DIVLTQSDDSLAVSLGERATISCKSSQSLNSRTENTLAYQQKRGCPPKLLIYWASTR	80
Dd	1	DIVLTQSPASLSLAVSIAGQARTISCRASKSV--STSGYSVMHWYQQKRPGLPKILYLASN	58
Oy	81	ESGVDRFSGSGSGTDFTLTITSSLOAEDVAVYYCYQSYNL-YTFGGGTVEIK	132
Dd	59	ESGVARRSGSGSGTDFTLNIHPVEEDNAITYCQHSHKELPPTFFGGGTKEIK	111
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RESULT	6		
ID	09UL77	PRELIMINARY;	PRT; 108 AA.
AC	09UL77;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Yu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RT	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035037; AAD56273.1; -.		
DR	HSSP; P01607; IREI.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_v.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; Igv; 1.		
FT	NON_TER	1	
FT	NON_TER	108	
SQ	SEQUENCE	108 AA; 11738 MW; C06681716CAD16f3 CRC64;	

	Query Match	55.7%	Score 379.5;	DB 4;	Length 108;	
	Best Local Similarity	66.4%;	Pred. No. 7e-33;			
	Matches 75; Conservative 15; Mismatches 16; Indels 7; Gaps 2;					
Oy	21 DIVLQSPDSLAVSLGEGEATISCKSSQSLSLRTEENTYLAWVQOKPGQPPLLIYMASTR 80					
	:      :  :   ::   :					
Dd	1 DIQMNTQSFSSLSASVGDRVTITCRASQSI-----SYLNMYQKPKGRAPNLLIYAASSL 54					
	:      :  :   ::   :					
Oy	81 ESGVDPRFSGSGSGTDFLTLLISSLOAEDEVAYYYCTQSYNL-VTFGGTKRVEIK 132					
	:      :  :   ::   :					
Dd	55 QSGVPSRRFSGSGSGTDFLTLLISSLPDEPFATFYCCQSYSTSWTFEGTKRVEIK 107					
	:      :  :   ::   :					
RESULT 7						
Q9UL78	PRELIMINARY; PRT; 109 AA.					
ID	Q9UL78					
AC	Q9UL78;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).					
OC	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCL_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=98277139; PubMed=9614934;					
RA	Yu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,					
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";					
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).					
DR	EMBL; AF035036; AAD56272.1; -.					
DR	HSSP; P80362; IWTU.					
DR	InterPro; IPR003006; IG_MHC.					
DR	InterPro; IPR003596; Ig_V.					
DR	Pfam; PF00047; Ig; 1.					
DR	SMART; SM00406; IGV; 1.					
FT	NON_TER 1					
FT	NON_TER 109					
SQ	SEQUENCE 109 AA; 11646 MW; 56f75c52ec7be197 CRC64;					
	Query Match	55.7%	Score 379;	DB 4;	Length 109;	
	Best Local Similarity	68.1%;	Pred. No. 7.9e-33;			
	Matches 77; Conservative 15; Mismatches 15; Indels 6; Gaps 2;					
Oy	21 DIVLQSPDSLAVSLGEGEATISCKSSQSLSLRTEENTYLAWVQOKPGQPPLLIYMASTR 80					
	:      :  :   ::   :					
Dd	1 ELVLNQSGTLISLPGERATLSCRASQSVSS-----YLAWYQKPKGAPNLLIYGASR 55					
	:      :  :   ::   :					
Oy	81 ESGVDPRFSGSGSGTDFLTLLISSLOAEDEVAYYYCTQSYNL-VTFGGTKRVEIK 132					
	:      :  :   ::   :					
Dd	56 ATGIDPRFSGSGSGTDFLTLLISRLEPEDCAVYYCQYGS SPLTFGGTKRVEIK 108					
	:      :  :   ::   :					
RESULT 8						
Q9UL79	PRELIMINARY; PRT; 108 AA.					
ID	Q9UL79					
AC	Q9UL79;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)					
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).					
OC	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCL_TaxID=9606;					

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5645F19724FB4E CRC64;

Query Match 55.1%; Score 375.5; DB 4; Length 108;
Best Local Similarity 67.3%; Pred. No. 1.9e-32;
Matches 76; Conservative 11; Mismatches 19; Indels 7; Gaps 2;

QY 21 DIVLTGSPDSLAVSLGERRATISCKSSOSLNSRTRENTYLAWYQKPGQPKLLIYMASTR 80
DB 1 DIVMTGSPSLASVSGDRYITICRASOGI-----SSYLAWYQKPGKAPKELLIYASTL 54

QY 81 ESGVPRFSGSGSGTDEFTLTISSLQAEADVAVYYCTOSYNL--YTFGGGTKEIK 132
DB 55 QSGVPRFSGSGSGTDEFTLTISLQSEDFATYYCQOYISPPFTFGGTKEIK 107

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC 09UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 54.8%; Score 373.5; DB 4; Length 108;
Best Local Similarity 67.5%; Pred. No. 3e-32;
Matches 77; Conservative 11; Mismatches 17; Indels 9; Gaps 3;

QY 21 DIVLTGSPDSLAVSLGERRATISCKSSOSLNSRTRENTYLAWYQKPGQPKLLIYMASTR 80
DB 1 DIVMTGSPSLASVSGDRYITICRASOGI-----SSYLAWYQKPGKAPKELLIYASTL 54

QY 81 ESGVPRFSGSGSGTDEFTLTISSLQAEADVAVYYCTOSYNL--YTFGGGTKEIK 132
DB 55 ESGVPRFSGSGSGTDEFTLTISSLQAEADVAVYYCTOSYNL--YTFGGGTKEIK 132
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DB 55 QSGVPRFSGSGSGTDEFTLTISSLQEPEDVATYYC-QKYNAPRFGGTKEIK 107

RESULT 10
Q9UL83 PRELIMINARY; PRT; 108 AA.
AC 09UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 54.7%; Score 372.5; DB 4; Length 108;
Best Local Similarity 67.5%; Pred. No. 3.9e-32;
Matches 77; Conservative 16; Mismatches 12; Indels 9; Gaps 3;

QY 21 DIVLTGSPDSLAVSLGERRATISCKSSOSLNSRTRENTYLAWYQKPGQPKLLIYMASTR 80
DB 1 EIVMTGSPATLSVSGERRATISCRASQVSSN-----LAWYQKPGQAPRLIYCASTR 54

QY 81 ESGVPRFSGSGSGTDEFTLTISSLQAEADVAVYYCTOSYNL--YTFGGGTKEIK 132
DB 55 ATGIPARFSGSGSGTDEFTLTISLQFEDFAVYYC-QHYNMWPTFGGTKEIK 107

RESULT 11
Q9UL86 PRELIMINARY; PRT; 109 AA.
AC 09UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
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Db      115  PFTFGSGTKLEVK  127
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RESULT 1.5

ID	PRELIMINARY;	PRT;	104 AA.
Q9JL82			
Q9JL82			

AC Q9JL827

DT	01-CCT-2000 (TREMBLrel. 15, Created)
DT	01-CCT-2000 (TREMBLrel. 15, Created)
DT	01-CCT-2000 (TREMBLrel. 15, Created)

Dt	01-FEB-2001
Df	01-OCT-2000
	(TREMBLER, 15, Last sequence update)

DI 01-DEC-2001 (11EMBLER. 19, last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION

DE (FRAGMENT) .  
DE AND MOON INTERNOCCIDENTAL LIGHT CHAIN VARIABLE REGION

Mus musculi

OC Eukaryota; Metazoa; C

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

OX NCBI\_TaxID=10090;

RN	[1]
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RP SEQUENCE FROM N.A.  
PC EMPATIN-PAI B/C.

RX	MEDLINE=20448942.
KC	SIRKALN-BALB/C;

RA  
MEDLINE-204402  
Malkiel S. J. Li

" T-Cell-dependent antibody response

RT streptococcal polysaccharide, N-acetyl-glucosamine

RT with cardiac myosin.";

RL Infect. Immun. 68:5803-5808(2000).

DR EMBL; AF206024; AAF69322.1; -.  
DR HSSB: P01607.1; PFI

DR HSSP; POLBU; IREL.  
DB Interpro: TPB003006; Tg MHC

DR InterPro: IPR003596;

DR Pfam; PF00047; Ig; 1

DR SMART; SM00406; IGV; 1.

ET	NON_TER	1	1
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FT	NON_TER	104	104
CO	SEQUENCE	104	113

SEQUENCE 104 AA; 113

Query Match

### Best Local Similarity

**Matches** 6

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30 SLAVSLGERATISCKSSQSLNSRTRENYLAWYQOKPGQPPKLLIYWASTRESGVPPDRFS 85

2 SI.PVSI.GDOASTSCBSSOSI.YHT-NGNTYI.HWYI.OKBOSBK.I.TYKYSNPBESCIVBRES 60

DD 2 3LFVSL0DQKAS1SCAKSSQSLVNI -NGONI LHMILEQKPGQSPALLEI KVSNKESGVFKES 00

QY 90 GSGSGTDFTLTISLSLOAEDVAVYYCTOSYNL-YTFGGGTKEIK 1322

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Search completed: August 26, 2002, 15:05:03

Job time: 367 sec

GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 26, 2002, 14:58:51 ; Search time 42.03 Seconds

(without alignments)  
348,840 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681  
Sequence: 1 MDSSQAVLILLILMLVSGTCG.....YCTGSYMLYFGGCTKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database : A.Genesec 032802:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	681	100.0	132	21	AA07966
2	629	92.4	132	21	AA07964
3	596	87.5	148	10	AA093078
4	592	86.9	239	16	AA076087
5	580.5	85.2	137	18	AA010545
6	575.5	84.3	137	18	AA010544
7	567.5	83.3	137	21	AA095243
8	559.5	82.2	133	15	AA059509
9	557.5	81.9	133	9	AA080894
10	557	81.8	134	18	AA06206
11	555.5	81.6	240	22	AA00815

12	555	81.5	141	20	AA24374	Human monoclonal a
13	553.5	81.3	135	21	AA03714	Immunoglobulin Kap
14	548	80.5	241	13	AA028609	Vector pMDR1007.
15	547.5	80.4	240	20	AA050161	Human reshaped F19
16	544.5	80.0	133	17	AA085909	Monoclonal antibody
17	544.5	80.0	134	20	AA050690	Human Hum4 VL Clat
18	539.5	79.2	133	15	AA048633	Human Hum4 VL Clat
19	539.5	79.2	134	14	AA030485	V kappa region of
20	538.5	79.1	137	18	AA010547	Wild type murine a
21	538.5	79.1	139	17	AA09469	Monoclonal antibody
22	534.5	78.5	137	18	AA021655	Chimeric Mab 15 PC
23	531.5	78.0	128	21	AA056734	Amino acid sequenc
24	531.5	78.0	134	13	AA025158	V-region of L-chain
25	530.5	77.9	137	18	AA021653	Mouse Mab 15 Light
26	528.5	77.6	133	21	AA090719	CC49 VL region pro
27	528.5	77.6	133	21	AA057051	Amino acid sequenc
28	528.5	77.6	133	22	AA002138	Mouse partial anti
29	528.5	77.6	134	14	AA08317	Sequence encoded b
30	525.5	77.2	133	20	AA050154	Murine monoclonal
31	525.5	77.2	240	20	AA050156	Chimeric mouse/hum
32	524.5	77.0	244	21	AA096305	Human IGFAM-17 Imm
33	522.5	76.7	134	22	AA074792	Anti-CA125 bifunct
34	519.5	76.3	154	21	AA053686	Human colon cancer
35	513.5	75.4	495	18	AA032480	Growth factor CATR
36	513.5	75.4	495	20	AA06908	CATR-REV aminoact
37	507.5	74.5	113	22	AA065565	Amino acid sequenc
38	504.5	74.1	113	20	AA050145	Antibody F19 human
39	503	73.9	113	22	AA062769	Human HIV-1 monocl
40	502.5	73.8	155	18	AA032483	Kappa light chain
41	502.5	73.8	155	20	AA06912	Human variable kap
42	502.5	73.8	342	18	AA032482	Growth factor TLHL
43	502.5	73.8	342	20	AA06909	TLHL amino acid se
44	500.5	73.5	113	20	AA050143	Antibody F19 human
45	498.5	73.2	113	15	AA050314	Humanised light ch

## ALIGNMENTS

RESULT	1
AA07966	standard; Protein; 132 AA.
AA07966;	
14-NOV-2000	(first entry)
A light chain variable region of humanised 3S1 antibody.	
Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;	
KW autoimmune disease; infectious disease; inflammatory disorder;	
KW systemic lupus erythematosus; diabetes mellitus; insulin; asthma;	
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;	
KW multiple sclerosis; transplant rejection; proliferative disease;	
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;	
KW aplastic anaemia; myeloid dysplasia syndrome.	
XX	
OS Synthetic.	
OS Mus sp.	
OS Homo sapiens.	
XX	
Key	Location/Qualifiers
Peptide	1..20
Protein	/note- "signal peptide"
	21..132
	/note- "mature protein"
Region	44..60
	/note- "complementarity determining region 1"
Region	76..82
	/note- "complementarity determining region 2"
Region	115..122
	/note- "complementarity determining region 3"

```

PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celinker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB: AAA59695.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 3; Fig 2B; 162pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC humanised murine antibody 3D1. The antibody has a binding specificity to
CC B7 molecules. The antibody is used to construct humanized
CC immunoglobulins, which comprise an antigen binding region of non-human
CC origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infectious
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 681; DB 21; Length 132;
Best Local Similarity 100.0%; Pred. No. 6,7e-47;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLIILWVGTCGDIIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 60
Db 1 mdsqagvlllllllwsqgtdglvltqspdslavslgeratiscskssqslnstrrenyla 60
QY 61 WYQOKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVYYCTQSYNL 120
Db 61 WYQKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVYYCTQSYNL 120
QY 121 YTFGQGTKEIK 132
Db 121 ytfgggtkveik 132
SQ Sequence 132 AA;

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KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..132
FT /note= "mature protein"
FT Region 44..60
FT /note= "complementarity determining region 1"
FT Region 76..82
FT /note= "complementarity determining region 2"
FT Region 115..122
FT /note= "complementarity determining region 3"
XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celinker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB: AAA59693.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 1; Fig 1B; 162pp; English.
XX
CC The present sequence represents the light chain variable region of the
CC murine antibody 3D1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non-human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulinitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 132 AA;

Query Match 92.4%; Score 629; DB 21; Length 132;
Best Local Similarity 90.9%; Pred. No. 8,8e-43;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSQAOVLILLIILWVGTCGDIIVLTQSPDSLAVSLGERATISCKSSQSLNSTRRENYLA 60
Db 1 mdsqagvlllllllwsqgtdglvltqspdslavslgeratiscskssqslnstrrenyla 60
QY 61 WYQOKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVYYCTQSYNL 120
Db 61 WYQKPGQPKLLIYWASTRESGVNPRFSGSGSGTFTLTITSSIAQEDVAVYYCTQSYNL 120
QY 121 YTFGQGTKEIK 132

```



KM variable region; detection; inhibition; mediation; cell adhesion;  
KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KM acute respiratory distress syndrome; gross cystic breast disease;  
KM cancer; treatment; splanchic occlusion shock; psoriasis;  
KM complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
DR WPI: 1997-077272/07.  
DR N-PSDB: AAT60730.  
XX  
XX  
PT Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
PS Claim 18; Page 71; 89pp; English.  
XX  
CC The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, acute cystic breast disease or cancer, or treat, e.g.  
CC splanchic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
CC  
XX  
SQ Sequence 137 AA;  
  
Query Match 85.2%; Score 580.5; DB 18; Length 137;  
Best Local Similarity 85.0%; Pred. No. 6.4e-39;  
Matches 113; Conservative 8; Mismatches 11; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLVSGTGDIVLTOSPSLAVSLGERATISCKSSOSILNSTRRENYLA 60  
Db 5 mesqfgyvmsllfwsqcgdiwmtqpsdlavslgeratlnckssqslhsqngknylt 64  
QY 61 WYQQRKGQPPKLLIYVASTRESGVPRFSGSGSGTFTLTIRISLQAEVAVVYCTQSYNL 120  
Db 65 WYQQRKGQPPKLLIYVASTRESGVPRFSGSGSGTFTLTIRISLQAEVAVVYCTQSYNL 124  
QY 121 -YTFGGGTVEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 6  
AAW10544  
ID AAW10544 standard; Protein; 137 AA.  
AC AAW10544;  
XX  
DT 25-SRP-1997 (first entry)  
XX  
DE Humanised murine anti-E-selectin antibody CY1788V(LA).

XX  
KM Humanised; murine; mouse; E-selectin; antibody; light chain;  
KM variable region; detection; inhibition; mediation; cell adhesion;  
KM diagnosis; reduction; inflammation; septic shock; ARDS; sepsis;  
KM acute respiratory distress syndrome; gross cystic breast disease;  
KM cancer; treatment; splanchic occlusion shock; psoriasis;  
KM complement; chimeric.  
XX  
OS Chimeric - Mus spp.  
OS Chimeric - Homo sapiens.  
OS Synthetic.  
XX  
PN WO9640942-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 06-JUN-1996; 96WO-US09204.  
XX  
PR 07-JUN-1995; 95US-0482112.  
XX  
PA (CYTE-) CYTEL CORP.  
XX  
PI Bendig MM, Jones ST, Perez C, Saldanha JW, Williams MA;  
PI Jones S;  
XX  
DR WPI: 1997-077272/07.  
DR N-PSDB: AAT60729.  
XX  
XX  
PT Humanised anti-E-selectin antibody - useful for diagnosis and  
PT treatment of, e.g. inflammatory responses, septic shock, acute  
PT respiratory distress syndrome or cancer  
XX  
PS Claim 17; Page 69; 89pp; English.  
XX  
CC The present sequence is the humanised murine anti-E-selectin  
CC antibody (Ab) light chain variable region, CY1788V(LA). The Ab can  
CC be used to detect E-selectin, or inhibit E-selectin mediated cell  
CC adhesion. It can also be used to diagnose, reduce or inhibit an  
CC inflammatory response, or the severity of pathologies, e.g. septic  
CC shock, acute respiratory distress syndrome, wound associated  
CC sepsis, acute cystic breast disease or cancer, or treat, e.g.  
CC splanchic occlusion shock, or psoriasis. It can be administered to  
CC a human without inducing an immune response, in addition, the  
CC effector portion of the Ab can interact with various components of  
CC the human immune system, including complement.  
CC  
XX  
SQ Sequence 137 AA;  
  
Query Match 84.5%; Score 575.5; DB 18; Length 137;  
Best Local Similarity 84.2%; Pred. No. 1.6e-38;  
Matches 112; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 MDSQAQVLLILLVSGTGDIVLTOSPSLAVSLGERATISCKSSOSILNSTRRENYLA 60  
Db 5 mesqfgyvmsllfwsqcgdiwmtqpsdlavslgeratlnckssqslhsqngknylt 64  
QY 61 WYQQRKGQPPKLLIYVASTRESGVPRFSGSGSGTFTLTIRISLQAEVAVVYCTQSYNL 120  
Db 65 WYQQRKGQPPKLLIYVASTRESGVPRFSGSGSGTFTLTIRISLQAEVAVVYCTQSYNL 124  
QY 121 -YTFGGGTVEIK 132  
Db 125 pltfqggtkveik 137  
  
RESULT 7  
AAW95243  
ID AAW95243 standard; Protein; 137 AA.  
AC AAW95243;  
XX  
DT 29-AUG-2000 (first entry)  
XX

XX Humanised antibody hucC49 light chain variable region.  
 DE Humanised antibody; monoclonal antibody; CC49; hucC49; CDR;  
 XX Complementarity determining region; mouse; human; carcinoma;  
 KM colon cancer; tumor associated glycoprotein-72; TAG-72;  
 KW tumor marker; diagnosis; therapy.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 44..59  
 FT /note= "CDR1"  
 FT Region 76..82  
 FT /note= "CDR2"  
 FT Region 115..123  
 FT /note= "CDR3"  
 FT  
 PN WO200026394-A1.  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US25552.  
 XX  
 PR 31-OCT-1998; 98US-0106534.  
 PR 02-NOV-1998; 98US-0106757.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Kashmiri SVS, Padlan EA, Schlom J;  
 DR WPI; 2000-365637/31.  
 XX  
 PT Chimeric variants of CC49 monoclonal antibodies useful for detecting  
 PT and treating cancers associated with the expression of the pancreaticoma  
 PT tumor-associated antigen TAG-72 -  
 XX  
 PS Disclosure: Fig 4; 76pp; English.  
 XX  
 CC The present sequence is that of the light chain variable region  
 CC (VL) of hucC49, a humanised monoclonal antibody (Mab) formed by  
 CC grafting hypervariable regions from murine Mab CC49 into VL and VH  
 CC frameworks of human MADS LEN and 21/28' CL, respectively, while  
 CC retaining murine framework residues required for integrity of the  
 CC antigen combining site structure. hucC49 binds to the human  
 CC pancreaticoma tumor associated glycoprotein-72 (TAG-72), which is  
 CC found on the surface of certain human tumours. The invention is  
 CC directed towards mouse-human chimeric variants of CC49 MADS with  
 CC minimal murine content, to methods of making such variants, and  
 CC their therapeutic application. The invention provides  
 CC complementarity determining region (CDR) variants of hucC49 in  
 CC which fewer than all 6 CDRs of CC49 are present, and specificity  
 CC determining region (SDR) variants of hucC49 in which only SDRs of  
 CC at least 1 CDR from CC49 are present. Particular variants of hucC9  
 CC have either L-CDR1 and/or L-CDR2 from human MAB LEN. These  
 CC variants have the same or 2-fold lower affinity constant than  
 CC hucC49. Other variants additionally have corresponding human  
 CC residues at position 97 of L-CDR3, and positions 60, 61, 62 and 64  
 CC of H-CDR2. The variants are used in claimed methods of treating  
 CC cancer and for detecting cancer cells that express TAG-72.  
 XX  
 SQ Sequence 137 AA:

Query Match 83.3%; Score 567.5; DB 21; Length 137;  
 Best Local Similarity 82.7%; Pred. No. 6.8e-38;  
 Matches 110; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

OY 1 MDSQAQVILLILLMWSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 DB 1 mdsqagvllmllllwsgtgddivmgsqpsdlavslgeratlsckssqsllysgnqnyla 60

OY 61 WYQOKPQGPRLIYMASTRESGVPPDRFSGSGGTDTLTITSSIQADVAIVYCTOSYNL 120  
 DB 61 wyqkpgqspklllywasaresgvpdrfsgsggttdltltssvgaedvavyycqgyysy 120  
 OY 121 -YTFGOSTKYEIK 132  
 DB 121 plftgagtkleik 133

RESULT 8  
 AAR59509  
 ID AAR59509 standard; Protein; 133 AA.  
 AC AAR59509;  
 XX  
 XX 31-DEC-1994 (first entry)  
 DT  
 DE Sequence of the light chain variable region of the mouse NA-8  
 DE antibody, including the signal sequence and mature chain.  
 XX  
 KM Antibody NA-8; human CD18; complementarity determining region; CDR;  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 21..133  
 FT /label= Mature light chain  
 FT  
 PN W09412214-A.  
 PD 09-JUN-1994.  
 XX  
 PF 30-NOV-1993; 93WO-US11611.  
 XX  
 PR 01-DEC-1992; 92US-0983949.  
 XX  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Co MS, Landolfi NF;  
 DR WPI; 1994-199973/24.  
 DR N-PSDB; AA066845.  
 XX  
 PT New humanised antibodies specific for CD18 - derived from new  
 PT murine antibody NA-8, prevent binding of neutrophils to  
 PT endothelial cells, useful for treating inflammation  
 XX  
 PS Disclosure: Fig 1A; 50pp; English.  
 XX  
 CC The mouse antibody NA-8 binds to human CD18. cDNAs for the heavy  
 CC chain and light chain variable domain genes of NA-8 were cloned  
 CC using anchored PCR. The cDNA variable domain sequences and the  
 CC deduced AA sequences are shown in AA066845/R59509 and AA066846/R59510.  
 XX  
 SQ Sequence 133 AA:

Query Match 82.2%; Score 559.5; DB 15; Length 133;  
 Best Local Similarity 80.5%; Pred. No. 2.8e-37;  
 Matches 107; Conservative 15; Mismatches 10; Indels 1; Gaps 1;

OY 1 MDSQAQVILLILLMWSGTGDIVLTQSPDSLAVSLGERATISCKSSQSLNSRTRENYLA 60  
 DB 1 mdsqagvllmllllwsgtgddivmgsqpsdlavsgelvmcsksqsllyssiqnyla 60

OY 61 WYQOKPQGPRLIYMASTRESGVPPDRFSGSGGTDTLTITSSIQADVAIVYCTOSYNL 120  
 DB 61 wyqkpgqspklllywasaresgvpdrfsgsggttdltltssvgaedvavyycqgyysy 120

OY 121 -YTFGOSTKYEIK 132  
 DB 121 plftgagtkleik 133

RESULT 9  
 AAP80894  
 ID AAP80894 standard; protein; 133 AA.  
 AC AAP80894;  
 DT 03-DEC-1990 (first entry)  
 DE V region of L chain of anti-P.aeruginosa exotoxin Ab #1.  
 XX  
 XX Pseudomonas aeruginosa; anti-exotoxin antibody; L chain; V region;  
 KM ds.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label=signal peptide  
 FT Region 21..133  
 FT /label=V region of L chain  
 XX  
 XX EP270077-A.  
 PD 08-JUN-1988.  
 XX  
 XX 01-DEC-1987; 87EP-0117760.  
 XX  
 XX 03-DEC-1986; 86JP-0288340.  
 PR 26-NOV-1987; 87JP-0298513.  
 XX  
 XX (SDMO ) SUMITOMO CHEM IND KK.  
 PA  
 PI Nakatani T, Nomura N, Horigome K, Noguchi H;  
 XX  
 XX MPI: 1988-156310/23.  
 DR N-PSDB; AAN80499.  
 XX  
 XX New gene encoding for antibody to Pseudomonas aeruginosa exotoxin -  
 PT plus recombinant vectors and host cells, useful for treating  
 PT infections.  
 PS  
 PS Claim 4; Page 25; 39pp; English.  
 XX  
 XX Sequence is variable region of light chain of anti-exotoxin  
 CC antibody with signal sequence. AAN80498 encodes the same sequence  
 CC except that its signal peptide-encoding sequence contains an  
 CC intron.  
 CC See also AAN80495-N80496, AAN80498 and AAN80941-2.  
 CC  
 XX  
 XX Sequence 133 AA;  
 SQ  
 Query Match 81.9%; Score 557.5; DB 9; Length 133;  
 Best Local Similarity 84.6%; Pred. No. 4.1e-37;  
 Matches 110; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

XX  
 AC AAM06206;  
 XX  
 DT 17-FEB-1997 (first entry)  
 XX  
 DE Xenograft antibody HAR-1 kappa light chain variable region.  
 XX  
 XX Xenograft rejection; xenotransplantation; organ transplant;  
 KW animal model; hamster; monoclonal antibody; HAR-1.  
 XX  
 OS Rattus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH Region 1..20  
 FT /label= Leader  
 FT Region 21..43  
 FT /label= FR-1  
 FT /note= "framework region 1"  
 FT Region 44..60  
 FT /label= CDR-1  
 FT /note= "complementarity determining region 1"  
 FT Region 61..75  
 FT /label= FR-2  
 FT /note= "framework region 2"  
 FT Region 76..82  
 FT /label= CDR-2  
 FT /note= "complementarity determining region 2"  
 FT Region 83..114  
 FT /label= FR-3  
 FT /note= "framework region 3"  
 FT Region 115..122  
 FT /label= CDR-3  
 FT /note= "complementarity determining region 3"  
 FT Region 123..134  
 FT /label= FR-4  
 FT /note= "framework region 4"  
 XX  
 PN WO9636358-A1.  
 XX  
 PD 21-NOV-1996.  
 XX  
 XX 14-MAY-1996; 96WO-US06804.  
 PR 15-MAY-1995; 95US-0440621.  
 XX  
 XX (CEDA-) CEDARS SINAI MEDICAL CENT.  
 PA  
 PI Cramer DV, Makowka L, Wu G;  
 XX  
 XX MPI: 1997-011852/01.  
 DR N-PSDB; AAT43415.  
 XX  
 XX Inhibiting xenograft rejection by modifying antigen expression of  
 PT the graft - prevents binding of anti-donor antibody and prolongs  
 PT graft survival  
 PT  
 XX  
 XX Claim 11; Page 99; 135pp; English.  
 PS  
 PS A polypeptide (AAM06206) comprises the kappa light chain variable  
 CC region of the LEW rat anti-hamster xenograft monoclonal antibody  
 CC HAR-1. It is encoded by a cDNA clone (AAT43415) obtd. from a HAR-1  
 CC hybridoma light chain cDNA library; the hybridoma was produced by  
 CC fusing spleen cells of a LEW rat that had received a hamster heart  
 CC transplant, with rat myeloma cells. Recombinant fragments, e.g.  
 CC Fab'2 and Fab', of the antibody block binding of preformed  
 CC anti-donor xenograft antibodies in a recipient animal serum to  
 CC antigen expressed by endothelial cells of the xenograft, i.e. they  
 CC inhibit antibody-mediated rejection, thereby prolonging the  
 CC survival of the hamster xenograft in the recipient.  
 CC  
 XX  
 XX Sequence 134 AA;  
 SQ



Query Match	81.8%	Score 557	DB 18	Length 134
Best Local Similarity	78.8%	Pred. No. 4.5e-37		
Matches 104	Conservative 14	Mismatches 14	Indels 0	Gaps 0
QY	1	MDSQAVLILLILWVSGTCGDIIVLTQSPDSLAVSGERATICKSSQSLNSTRDENYIA	60	
Db	1	mesqcvimslilwvsgtcgdiwctqpsqsgavagckvwmckssqsllynenknyla	60	
QY	61	WYQKPGQPPKLLIYMASRREGGVDRPFGSGSGNDFTLTISLQAEYAVYCCQSYNL	120	
Db	61	wyrqpgqgsklllymasrcresgvpdrfttqsgsgdftltlssvaedlavyyccqyyyl	120	
QY	121	YTFGGGTKEVEIK	132	
Db	121	ytfgggtkvek	132	
RESULT 11				
ID	AAU00815	standard; Protein; 240 AA.		
XX	AAU00815;			
XX	01-JUN-2001	(first entry)		
DE	Human	Immunoglobulin superfamily, IgSF, protein #1.		
XX	Human	Immunoglobulin superfamily protein; IgSF; Immune response;		
KW		inflammatory response; cell-cell interaction; cell-surface recognition;		
KW		neural disorder; immune system disorder; muscular disorder;		
KW		cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;		
KW		cancer; common variable adhesion deficiency syndrome; AIDS; SCID;		
KW		acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;		
KW		Alzheimer's disease; Crohn's disease; liver cancer; leukemia;		
KW		Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;		
KW		atherosclerosis; stroke; diabetes mellitus; Addison's disease;		
KW		urticaria; severe combined immunodeficiency; antibody.		
XX	Homo sapiens.			
XX	OS			
XX	Key	Location/Qualifiers		
FT	Region	52..58	/label=	Immunogenic_epitope
FT	Region	63..70	/label=	Immunogenic_epitope
FT	Region	79..90	/label=	Immunogenic_epitope
FT	Region	118..126	/label=	Immunogenic_epitope
FT	Region	146..154	/label=	Immunogenic_epitope
FT	Domain	160..240	/label=	Immunogenic_epitope
FT	Region	183..199	/label=	Immunoglobulin_like_domain
FT	Region	209..215	/label=	Immunogenic_epitope
FT	Region	233..240	/label=	Immunogenic_epitope
FT	Region		/label=	Immunogenic_epitope
XX	WO200118176-A1.			
XX	15-MAR-2001.			
XX	29-AUG-2000;	2000WO-US23662.		
XX	03-SEP-1999;	99US-0152248.		
XX	(HUMA-)	HUMAN GENOME SCI INC.		
XX	(NTU/)	NT J.		
XX	Young PE,	Ruben SM,	Shi Y,	

XX	WPI: 2001-203084/20.
DR	N-PSDB; AAS001445.
XX	
PT	Isolated nucleic acid molecule encoding a human secreted protein is
PT	used in preventing, treating or ameliorating a medical condition -
XX	
PS	Claim 11; Page 237; 247pp; English.
XX	
CC	The sequence is a human Immunoglobulin superfamily, IgSF, protein,
CC	a diverse family of proteins involved in cell-cell interactions,
CC	cell-surface recognition, intercellular communication and immune and
CC	inflammatory responses. Polypeptides and antibodies directed to
CC	polypeptides of the present invention are useful to provide immunological
CC	probes for differential identification of tissues. Antibodies can be
CC	used to assay levels of polypeptides encoded by polynucleotides of the
CC	invention. Polypeptides of the present invention can be used to treat
CC	or prevent diseases or conditions such as neural disorders, immune
CC	system disorders, muscular disorders, reproductive disorders,
CC	gastrointestinal disorders, pulmonary disorders, cardiovascular
CC	disorders, renal disorders, proliferative disorders, and/or cancerous
CC	diseases and conditions. Polynucleotides of the invention are also
CC	useful in treating the above disorders. Examples of the disorders
CC	include common variable adhesion deficiency syndrome, acquired
CC	immunodeficiency syndrome (AIDS), anaemia, Rheumatoid arthritis,
CC	Alzheimer's disease, Crohn's disease, liver cancer, leukaemia, Hodgkin's
CC	lymphoma, Parkinson's disease, Huntington's disease, dementia,
CC	atherosclerosis, stroke, diabetes mellitus, Addison's disease,
CC	urticaria, severe combined immunodeficiency (SCID). Many more
CC	examples of diseases and disorders are given in the specification.
XX	
SQ	Sequence 240 AA:
	Query Match 81.6%; Score 555.5; DB 22; Length 240;
	Best Local Similarity 83.1%; Pred. No. 1,1e-36;
	Matches 108; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
QY	4 QAOVILLLLWVGTCGDIVLTQSPDSLAVSLGERATTSCKSSQSLNSRTRENTLAWYQ 63
	1 1
DB	4 qcvfvislllwisgagdydvtmctpsdsvslsgeratlnckssqcvlyssdknylawyq 63
QY	64 OKRGPDPKLLIYWASTRESGVDPFRSGSGSGNDPFLTSSLOAEVAVYYCQSQNL- 122
	1 1
DB	64 qkpqpqpklllywastresgvpdrrtsqsgsgdfcltlsslqaedvayyccqysstyps 123
QY	123 FQGQTKVEIK 132
	1 1
DB	124 fsgqtkleik 133
RESULT 12	
AAV24374	
ID	AAV24374 standard; Protein; 141 AA.
XX	
AC	AAV24374;
XX	
DT	17-SEP-1999 (first entry)
XX	
DE	Human monoclonal antibody against CTGF SEQ ID NO:16.
XX	
KW	Human: monoclonal antibody; connective tissue growth factor; CTGF;
KW	cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
KW	skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
KW	rheumatic vascular inflammation.
XX	
OS	Homo sapiens.
XX	
PN	WO933878-A1.
XX	
PD	08-JUL-1999.
XX	
PF	16-DEC-1998; 98WO-JP05697.



```
XX WO9209305-A.
PN
XX 11-JUN-1992.
PD
XX 27-NOV-1991; 91WO-US08843.
PF
XX 27-NOV-1990; 90US-0618542.
PR
XX (BIOJ ) BIOGEN INC.
PA
XX Burkly LC, Chisholm PL, Rosa JJ, Rosa MD, Thomas DW;
PI
XX WPI: 1992-39839/48.
DR
XX N-PSDB: AAQ30920.
DR
XX
XX New anti-CD4 antibody homologues - which bind CD4, do not block
PT binding of HIV gp120 to CD4 but block HIV-induced syncytia
PR formation between CD4+ cells
PT
XX
XX Disclosure: Page 166-7; 205pp; English.
PS
XX
XX The sequence given is encoded by the insert of the vector pMDR1007.
CC pMDR1006 (see AAQ30919) and pSAB132 (see AAQ30906) were used in the
CC construction of this vector. Three fragments were ligated together
CC to generate pMDR1006; a 572 bp fragment of pMDR85 (see AAQ30913), a
CC 3442bp ActI/EcoRV fragment of pMDR986 (see AAQ30918) and a 326 bp
CC EcoRV/BglII fragment of pMDR1003 (see AAQ30900). The ligation mixture
CC was used to transform E. coli JA221(Iq) to ampicillin resistance.
CC pMDR1006 was cleaved with NotI and the 1693 bp fragment isolated was
CC ligated into NotI linearised pSAB132 which had been dephosphorylated
CC by calf alkaline phosphatase. This generates the plasmid pMDR1007.
CC The dephosphorylated mixture was fractionated through low temperature
CC melting agarose and used to transform E. coli JA221(Iq) to ampicillin
CC resistance. The pMDR1007 insert comprises DNA encoding, in a 5' to 3'
CC order, the immunoglobulin kappa chain signal peptide, amino acid (AA)
CC 1-AA112 of the humanised 5A8 light chain variable region (LV) followed
CC by genomic DNA encoding AA108-AA214 of the human kappa light chain,
CC ie. the light chain constant region (LC). This polypeptide is an
CC antibody homolog which was shown to bind to CD4 but did not block the
CC binding of gp120 to CD4. CD4 is a cell surface glycoprotein of CD4+
CC lymphocytes (helper/inducer cells). The homolog blocked HIV-induced
CC syncytia formation. This homolog can be used in the detection,
CC prophylaxis and treatment of diseases caused by infective agents whose
CC primary targets are CD4+ cells.
CC
XX
XX Sequence 241 AA:
SQ
XX
XX
XX Query Match 80.5%; Score 548; DB 13; Length 241;
XX Best Local Similarity 83.6%; Pred. No. 4.1e-36;
XX Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;
```

```
XX
DE Human reshaped F19 antibody light chain (version a).
XX
XX Antibody: monoclonal; F19; fibrinogen activation protein alpha; PAP;
XX humanisation; complementarity determining region; CDR; CDR grafting;
XX reshaped; reactive stroma; fibroblast; epithelial cancer;
XX diagnosis; immune response; framework sequence; constant region;
XX variable region; producibility; treatment; cancer; colorectal; lung;
XX breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis;
XX detection; wound healing; skin inflammation; tumour; immunogenicity;
XX chimeric; light chain.
XX
XX Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
OS
XX
XX Key
FH Location/Qualifiers
FT 1..20
FT /note= "Leader peptide"
FT Protein
FT 21..240
FT /note= "Mature human reshaped F19 light chain"
FT Region
FT 21..140
FT /note= "Mature reshaped human F19 light chain variable
FT region"
FT Region
FT 44..60
FT /note= "Complementarity determining region (CDR) 1"
FT Region
FT 76..82
FT /note= "CDR 2"
FT Region
FT 115..123
FT /note= "CDR 3"
FT Region
FT 141..240
FT /note= "human kappa light chain constant region"
XX
XX EP953639-A1.
XX
XX 03-NOV-1999.
XX
XX 30-APR-1998; 98EP-0107925.
XX
XX 30-APR-1998; 98EP-0107925.
XX
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
XX
XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
XX Rettig WJ;
XX
XX WPI: 1999-621833/54.
XX N-PSDB: AA232784.
XX
XX New antibody protein, useful for treating cancer and for imaging
XX presence of activated stromal fibroblasts in healing wound or inflamed
XX skin -
XX
XX Example 3; Fig 30; 143pp; English.
XX
XX This sequence represents the light chain (version a) of a reshaped human
XX F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
XX antibody against fibroblast activation protein alpha (FAP). FAP is a cell
XX surface molecule of reactive stromal fibroblasts, and its induction
XX is a highly consistent molecular trait of the reactive stroma of many
XX types of epithelial cancer. Although F19 may be useful in vitro, e.g.,
XX for diagnosis, its applications for in vivo use in humans are problematic
XX as it elicits a human anti-mouse response which reduces the efficacy of
XX the antibody in patients and impairs continued administration. The
XX novel human reshaped F19 was humanised by grafting the murine
XX complementarity determining regions (CDRs) of F19 onto human variable
XX region framework sequences, and then joining these "reshaped human"
XX variable regions to human constant regions. These modifications
XX also result in the improved producibility in eukaryotic cell culture
XX systems as compared to a chimeric antibody having the entire variable
XX regions of F19 joined to human constant regions. The human reshaped F19
XX antibody has low immunogenicity for humans and is useful for treating
XX cancers e.g., colorectal cancers, non-small cell lung cancers, breast
XX cancers, head and neck cancers, ovarian cancers, lung cancers, bladder
XX
```



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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:00:19 ; Search time 20.74 Seconds

(without alignments)  
155,457 Million cell updates/sec

Title: US-09-249-011-8

Perfect score: 681

Sequence: 1 MDSQAQVLLILLMWSTGTCG.....YCTOSTYLNLYTFGGTKVEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/PCRTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	86.9	239	1	US-08-353-400-37
2	553.5	81.3	135	3	US-08-812-586-46
3	548.5	80.5	133	3	US-08-463-903-4
4	548.5	80.5	133	4	US-07-935-695-4
5	548	80.5	241	2	US-07-916-098A-56
6	528.5	77.6	133	2	US-08-822-028-12
7	528.5	77.6	133	3	US-08-479-285-12
8	526.5	77.3	133	5	PCR-US93-11611-2
9	522.5	76.7	154	3	US-08-513-968-36
10	513.5	75.4	495	3	US-08-828-741B-4
11	513.5	75.4	495	4	US-09-160-567-4
12	512.5	75.3	133	4	US-08-579-378A-2
13	512.5	75.3	133	5	PCR-US93-11612-2
14	512.5	73.8	113	4	US-08-525-539A-80
15	502.5	73.8	155	3	US-08-828-741B-11
16	502.5	73.8	155	4	US-09-160-567-11
17	502.5	73.8	342	3	US-08-828-741B-6
18	502.5	73.8	342	4	US-09-160-567-6
19	500.5	73.5	114	4	US-09-025-769B-17
20	498.5	73.2	113	5	PCR-US93-08435-8
21	498.5	73.2	275	3	US-08-463-903-6
22	498.5	73.2	275	4	US-07-935-695-6
23	497.5	73.1	115	4	US-09-025-769B-31
24	497.5	73.1	115	4	US-09-025-769B-49
25	496.5	72.9	114	1	US-08-360-125-6
26	496.5	72.9	114	2	US-08-450-578-6
27	496.5	72.9	114	2	US-09-017-628-6

28	496.5	72.9	114	2	US-09-014-880-6	Sequence 6, Appl
29	496	72.8	112	1	US-07-942-245-30	Sequence 30, Appl
30	494.5	72.6	171	3	US-08-463-903-20	Sequence 20, Appl
31	494.5	72.6	171	4	US-07-935-695-20	Sequence 20, Appl
32	494	72.5	114	4	US-08-929-856-66	Sequence 66, Appl
33	491.5	72.2	134	5	PCT-US93-11611-9	Sequence 9, Appl
34	490.5	72.0	113	5	PCT-US93-08435-6	Sequence 6, Appl
35	490	72.0	219	1	US-08-353-400-34	Sequence 34, Appl
36	489.5	71.9	285	3	US-08-463-903-22	Sequence 22, Appl
37	489.5	71.9	285	4	US-07-935-695-22	Sequence 22, Appl
38	488.5	71.7	134	4	US-08-718-323A-4	Sequence 4, Appl
39	487.5	71.6	260	3	US-08-463-903-2	Sequence 2, Appl
40	487.5	71.6	260	4	US-07-935-695-2	Sequence 2, Appl
41	487	71.5	288	4	US-09-423-439-38	Sequence 38, Appl
42	487	71.5	673	4	US-09-423-439-32	Sequence 32, Appl
43	485.5	71.3	113	1	US-08-467-420A-21	Sequence 21, Appl
44	485.5	71.3	113	1	US-08-470-110A-21	Sequence 21, Appl
45	485.5	71.3	113	1	US-08-667-769A-21	Sequence 21, Appl

## ALIGNMENTS

RESULT 1  
US-08-353-400-37  
Sequence 37, Application US/08353400  
Patent No. 5665357  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 37  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (ERO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/353,400  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9324819.3  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9411089.7  
FILING DATE: 03-JUN-1994  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-400-37

Query Match 86.9%; Score 592; DB 1; Length 239;  
Best local similarity 84.8%; Pred. No. 4.5e-48;

Matches 112; Conservative 11; Mismatches 9; Indels 0; Caps 0;

QY 1 MDSQAQVLLILLMWSTGCGIVITQSPDSLAVSLGERATISCKSSQSLNSRRRENTLA 60  
|||||  
DB 1 MDSQAQVLLILLMWSTGCGIVMSQSPSSLAAGKVTYMSCKSSQSLNSRRRKNLA 60  
QY 61 WYQOKPOPKLLIYMASTRESGVDRFSGSGSTDFLTITSSLOAEDVAVYCTQSYNL 120  
|||||  
DB 61 WYQOKPOPKLLIYMASTRESGVDRFSGSGSTDFLTITSSVQADLAITYCKQSYTL 120  
QY 121 YTFGGTKVEIK 132  
|||||  
DB 121 YTFGGTKVEIK 132

```

RESULT      2
US-08-812-586-46
; Sequence 46, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-812-586-46

Query Match      81.3%; Score 553.5; DR 3; Length 135;
Best Local Similarity 84.6%; Pred. No. 9,3e-45;
Matches 110; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY      4 QAAVILLLLLVSGTGTGDIATQSPDPLAVSLGERATISCKSSQSILNSFTRENYLAWYQ 63
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      4 QTQVTSLLMTLSGAAGDLVMNQSPDSLAVSLGERATINKSSQSILYSSNNKRYLWYQ 63

QY      64 QKGGPPKKLIYWASTREGSGVPDRFSGSGSGTDFTLTITSSLAQEDVAVVYYCTQSYNF-YT 122
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      64 QKPGGPPEKLIYWASTREGSGVPDRFSGSGSGTDFTLTITSSLAQEDVAVVYYCQQQSYTPPM 123

QY      123 FGQGTRKEIK 132
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      124 FGQGTKEIK 133

RESULT      3
US-08-463-903-4
; Sequence 4, Application US/08463903
; Patent No. 6071515
; GENERAL INFORMATION:
; APPLICANT: Mezes, Peter S.
; APPLICANT: Richard, Ruth A.
; APPLICANT: Affholter, Joseph A.
; APPLICANT: Kotite, Nicolas J.
; TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
; CURRENT APPLICATION NUMBER: US/08/463,903
; CURRENT FILING DATE: 1995-06-05

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EARLIER APPLICATION NUMBER: US 07/935,695
EARLIER FILING DATE: 1992-08-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 4
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from prL1001
LOCATION: 1..133
US-08-463-903-4

Query Match      80.5%; Score 548.5; DB 3; Length 133;
Best Local Similarity 83.8%; Pred. No. 2.7e-44;
Matches 109; Conservative 6; Mismatches 14; Indels 1; Gaps 1.

QY 4 QAOVILLILMLWSTGCGIVLTPSPDSLAVSLGERATISCKSSOSILNSRPRENYLAWQ 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 QTOVLSILLMTISGLAVGDIWMTQSPDSLAVSLGERATINCKSSQSVLSNNKNYLAWQ 63
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 64 QKPGPPKLLIYWASTRESGVDPDRSGSGGTDFLLTISLDAEDVAVYYCTQSYNL-IT 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 QKPGPPKLLIYWASTRESGVDPDRSGSGGTDFLLTISLDAEDVAVYYCOOYYSTPLT 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 123 FGQGTFRVEIK 132
   | | | | | | | |
Db 124 FGGGTKVVIK 133

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Query Match	Best Local Similarity	Matches 109; Conservative	Score 548.5; DB 4; Length 133;
80.5%;	83.8%;	6; Mismatches 14; Indels 1;	Gaps 1;
US-07-935-695-4	US-07-935-695-4	US-07-935-695-4	US-07-935-695-4
Sequence 4, Application US/07935695	Sequence 4, Application US/07935695	Sequence 4, Application US/07935695	Sequence 4, Application US/07935695
Patent No. 6329507	Patent No. 6329507	Patent No. 6329507	Patent No. 6329507
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Mezes, Peter S.	APPLICANT: Mezes, Peter S.	APPLICANT: Mezes, Peter S.	APPLICANT: Mezes, Peter S.
APPLICANT: Richard, Ruth A.	APPLICANT: Richard, Ruth A.	APPLICANT: Richard, Ruth A.	APPLICANT: Richard, Ruth A.
APPLICANT: Affholter, Joseph A.	APPLICANT: Affholter, Joseph A.	APPLICANT: Affholter, Joseph A.	APPLICANT: Affholter, Joseph A.
APPLICANT: Kolite, Nicolas J.	APPLICANT: Kolite, Nicolas J.	APPLICANT: Kolite, Nicolas J.	APPLICANT: Kolite, Nicolas J.
TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides	TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides	TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides	TITLE OF INVENTION: Dimer and Multimer Forms of Single Chain Polypeptides
FILE REFERENCE: 40224A US	FILE REFERENCE: 40224A US	FILE REFERENCE: 40224A US	FILE REFERENCE: 40224A US
CURRENT APPLICATION NUMBER: US/07/935,695	CURRENT APPLICATION NUMBER: US/07/935,695	CURRENT APPLICATION NUMBER: US/07/935,695	CURRENT APPLICATION NUMBER: US/07/935,695
CURRENT FILING DATE: 1992-08-21	CURRENT FILING DATE: 1992-08-21	CURRENT FILING DATE: 1992-08-21	CURRENT FILING DATE: 1992-08-21
PRIOR APPLICATION NUMBER: US 08/463,903	PRIOR APPLICATION NUMBER: US 08/463,903	PRIOR APPLICATION NUMBER: US 08/463,903	PRIOR APPLICATION NUMBER: US 08/463,903
PRIOR FILING DATE: 1995-06-05	PRIOR FILING DATE: 1995-06-05	PRIOR FILING DATE: 1995-06-05	PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 102	NUMBER OF SEQ ID NOS: 102	NUMBER OF SEQ ID NOS: 102	NUMBER OF SEQ ID NOS: 102
SOFTWARE: MS-Word for Windows, Ver. 7.0	SOFTWARE: MS-Word for Windows, Ver. 7.0	SOFTWARE: MS-Word for Windows, Ver. 7.0	SOFTWARE: MS-Word for Windows, Ver. 7.0
SEQ ID NO 4	SEQ ID NO 4	SEQ ID NO 4	SEQ ID NO 4
LENGTH: 133	LENGTH: 133	LENGTH: 133	LENGTH: 133
TYPE: PRT	TYPE: PRT	TYPE: PRT	TYPE: PRT
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
FEATURE:	FEATURE:	FEATURE:	FEATURE:
NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001	NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001	NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001	NAME/KEY: Human kappa subgroup IV VL (Hum4 VL) from pRL1001
LOCATION: 1..133	LOCATION: 1..133	LOCATION: 1..133	LOCATION: 1..133
US-07-935-695-4	US-07-935-695-4	US-07-935-695-4	US-07-935-695-4

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RESULT      6
US-07-916-098A-56
Sequence 56, Application US/07916098A
Patent No. 5871732
GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & MITCHELL, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match          80.5%   Score 548; DB 2; Length 241;
Best Local Similarity 83.6%; Pred. No. 5,8e+44;
Matches 107; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY    5 AOVLLILLVWSGTCGDIVLTQSPDSLAVSLGERATTSCKSSQSILNSRTRENYLAWYQQ 64
      ||| ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    7 AOLGLILLMPGARGDVTMTQSPDSLAVSLGERATINCCKSSGSILYSTNQKNYLAWYQQ 66

QY    65 KPGQPRLIIYWASTRESGVDPDRFGSGSGNDFTLTISLAQEDVAAYYYCCQSYNLTFEG 124
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    67 KPQGPRLIIYWASTRESGVDPDRFGSGSGNDFTLTISLAQEDVAAYYYCCQSYSYRTEG 126

QY    125 QGTVEIK 132
      :|||:|||
Db    127 RGTKLEIK 134
      :|||:|||

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US-08-822-028-12
: Sequence 12, Application US/08822028
: Patent No. 5993813
: GENERAL INFORMATION:
: APPLICANT: MEZES, PETER S
: APPLICANT: GOURLIE, BRIAN B
: APPLICANT: RIXON, MARK W
: APPLICANT: ANDERSON, WH KERR
: APPLICANT: KAPLAN, DONALD A
: APPLICANT: SCHOLOM, JEFFREY
: TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
: TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
: NUMBER OF SEQUENCES: 74
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DUANE C ULMER
: STREET: P. O. BOX 1967
: CITY: MIDLAND
: STATE: MICHIGAN
: COUNTRY: USA
: ZIP: 48641-1967
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/822.028
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/040.687
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: ULMER, DUANE C
: REGISTRATION/DOCKET NUMBER: 34,941
: REFERENCE/DOCKET NUMBER: C-37,075C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (517) 636-8104
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 133 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-822-028-12

Query Match 77.6%; Score 528.5; DB 2; Length 133;
Best Local Similarity 75.9%; Pred. No. 2e-42;
Matches 101; Conservative 16; Mismatches 15; Indels 1; Gaps 1;

QY 1 MDSQAIVLLLLLMWSGTCGDIVLTQSPDSLAVSLGERATICKSKSQSLNSRTRENYIA 60
Db 1 MDSQAIVLLLLLMWSGTCGDIVMSQSPSSLPVSVEKVTLLCKSSQSILYSGNOMNYIA 60
QY 61 WYQQKPGQSPKRLIYWASRRESGVDPDRFSGSGSTGTFTLTISLAEDVAVYYCTQSYNL 120
Db 61 WYQQKPGQSPKRLIYWASRRESGVDPDRFTGSGSTGTFTLTISSVKTEDLAVYYCQQTYSY 120
QY 121 -YTFGGGTKEVETK 132
Db 121 PLTFGAGTKLVLK 133

RESULT 7
US-08-479-285-12
: Sequence 12, Application US/08479285
: Patent No. 6207815
: GENERAL INFORMATION:
: APPLICANT: MEZES, PETER S
: APPLICANT: GOURLIE, BRIAN B
: APPLICANT: RIXON, MARK W
: APPLICANT: ANDERSON, WH KERR

```











